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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/522,753	03/10/2000	Ronald M. Evans	SALK1510-3	4924

30542 7590 05/23/2005

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SAN DIEGO, CA 92138-0278

EXAMINER

LEFFERS JR, GERALD G

ART UNIT	PAPER NUMBER
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1636

DATE MAILED: 05/23/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary

Application No.

09/522,753

Applicant(s)

EVANS ET AL.

Examiner

Gerald G. Leffers Jr., PhD

Art Unit

1636

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 15 February 2005.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 3-5, 9-10, 12-14, 16-25 & 38 is/are pending in the application.
- 4a) Of the above claim(s) _____ is/are withdrawn from consideration.
- 5) ☒ Claim(s) 9, 10, 12, 13, 17 and 38 is/are allowed.
- 6) ☐ Claim(s) 4, 5, 14, 16, 18, 19, 21-25 is/are rejected.
- 7) ☒ Claim(s) 3 and 20 is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
- ☐ Certified copies of the priority documents have been received.
 - ☐ Certified copies of the priority documents have been received in Application No. _____.
 - ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- 1) ☒ Notice of References Cited (PTO-892)
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☐ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date _____

- 4) ☐ Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____
- 5) ☐ Notice of Informal Patent Application (PTO-152)
- 6) ☒ Other: Exhibit A (Search Report SEQ ID No: 5)

DETAILED ACTION

Response to Amendment

Receipt is acknowledged of a supplementary response, filed 2/15/2005, in which the response explicitly answered each of the grounds of rejection made in the previous office action mailed on 4/20/2004. In the original response to the previous office action, filed on 8/12/2004, several claims were amended (claims 4, 5, 9, 12, 14, 23 and 25). Claims 3-5, 9-10, 12-14, 16-25 & 38 are pending and under consideration in the instant application.

Any rejection of record not addressed herein is withdrawn. This action is not final as there are new grounds of rejection presented herein that were not necessitated by applicants' amendment of the claims in the response filed on 8/12/2004.

Priority

Applicant has not complied with one or more conditions for receiving the benefit of an earlier filing date under 35 U.S.C. 120 as follows:

The later-filed application must be an application for a patent for an invention which is also disclosed in the prior application (the parent or original nonprovisional application or provisional application); the disclosure of the invention in the parent application and in the later-filed application must be sufficient to comply with the requirements of the first paragraph of 35 U.S.C. 112. See *Transco Products, Inc. v. Performance Contracting, Inc.*, 38 F.3d 551, 32 USPQ2d 1077 (Fed. Cir. 1994). The prior application to which the instant application seeks priority is U.S. Application Serial No. 08/522,726, filed 9/1/1995 (now U.S. Patent No. 6,489,441). The '726 application discloses only 3 sequences that correspond to SEQ ID NOS: 1-

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3 of the instant application. Each of the pending claims is directed to an isolated polynucleotide that (i) has a recited percent identity to one of SEQ ID NOS: 4, 6, & 8; or (ii) encodes a polypeptide having a recited percent identity to one of SEQ ID NOS: 5, 7 & 9. The prior application does not disclose these particular sequences. Therefore, the prior application does not provide support for the broadly recited genus of polynucleotides encompassed by the pending claims. Accordingly, the priority date for the pending claims is the filing date of the instant application (3/10/2000).

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 4, 19, 21-22 are rejected under 35 U.S.C. 102(b) as being anticipated by Chen et al (Nature, October 1995, Vol. 377, No. 6548, pages 454-457; see the entire reference). **This is a new rejection.**

Chen et al teach the identification and characterization of a transcriptional co-repressor that is an SMRT (i.e. silencing mediator for retinoid and thyroid hormone receptors). The SMRT polypeptide taught by Chen et al is encoded by a polynucleotide sequence that encodes a polypeptide that is ~94% identical to the sequence of SEQ ID NO: 5 (see the attached Exhibit A,

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result #6 for accession number HSU37146). Thus, the polynucleotide sequence taught by Chen et al anticipates the broad genus of polynucleotides encompassed by the instant claims.

Claims 4, 19, 21-22 are rejected under 35 U.S.C. 102(a) as being anticipated by Ordentlich et al (PNAS USA, 16 March 1999, Vol. 96, No. 6, pages 2639-2644; see the entire reference). **This is a new rejection.**

Ordentlich et al teach unique forms of the human and mouse nuclear receptor co-repressor SMRT. In particular, Ordentlich et al teach nucleic acids, described by accession numbers AF113003 & AF113001, that encode polypeptides with 100% & 88.2% identity with SEQ ID NO: 5, respectively (e.g. see results 1 & 3 of the search report provided as Exhibit A).

Claims 4, 19, 21-22 are rejected under 35 U.S.C. 102(a) as being anticipated by Park et al (PNAS USA, 30 March 1999, Vol. 96, No. 7, pages 3519-3524; see the entire reference). **This is a new rejection.**

Park et al teach the identification of an extended isoform of SMRT termed SMRTe by the authors. In particular, Park et al teach nucleic acids, described by accession numbers AF125672 & AF125671, that encode polypeptides with ~98% and ~82% identity with SEQ ID NO: 5 (e.g. see results 2 & 4 of the search report provided as Exhibit A).

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it

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pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 5 & 18 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. **This is a new rejection.**

Claim 5 is directed to an isolated polynucleotide encoding an SMRT co-repressor, or a peptide portion thereof, where the SMRT co-repressor or peptide portion thereof is capable of mediating the transcriptional silencing of at least one member of the steroid/thyroid hormone superfamily of receptors. The claim then recites the limitation of "...wherein said SMRT co-repressor or peptide portion thereof is encoded by a polynucleotide having at least 80% sequence identity with SEQ ID NO: 4". This latter recitation appears to specify that the polynucleotide having at least 80% identity to SEQ ID NO: 4 is a different polynucleotide from the one that is actually claimed. As such, the nucleotide that is actually claimed can be any nucleotide that encodes the same SMRT protein, or portion thereof, that is encoded by the second nucleotide sequence (e.g. the first polynucleotide encodes the SMRT protein, or portion thereof, and which is different from the second polynucleotide because of the degeneracy of the genetic code and/or because the two different polynucleotides comprise additional, different sequences from one another). There does not appear to be support anywhere in the originally filed specification or claims for this formulation. Therefore, the phrase "...wherein said SMRT co-repressor or peptide portion thereof is encoded by a polynucleotide having at least 80% sequence identity with SEQ ID NO: 4" is impermissible NEW MATTER.

Claims 23-25 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

This is a new rejection necessitated by applicants' amendment of the claims in the response filed on 8/12/2004.

Claim 23 is directed to a genus of oligonucleotides that are identifiable under "suitable stringency conditions" with respect to other nucleic acid sequences. The term "suitable stringency conditions" is used in the context of an identified oligonucleotide comprising at least 15 nucleotides that hybridizes to a polynucleotide of claim 4, but not to a polynucleotide encoding SEQ ID NO: 11 or to a polynucleotide encoding an amino acid sequence consisting of amino acids 1031 to 2517 of SEQ ID NO: 5. The specification does not define these exact conditions and the skilled artisan has no basis to visualize what these "suitable" conditions might be. Similarly, claim 25 specifies that the oligonucleotide of claim 23 hybridizes under "suitable stringency conditions" to a polynucleotide encoding SEQ ID NO: 5 or SEQ ID NO: 7, but does not hybridize to a polynucleotide encoding SEQ ID NO: 9. Again, the exact hybridization conditions are not described. Thus, the rejected claims comprise a genus of oligonucleotides that must meet very particular hybridization requirements, yet there is no description of the hybridization conditions that will necessarily identify an oligonucleotide having the recited functional activity.

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There does not appear to be any literal or implicit support in the originally filed claims or specification for claiming an isolated oligonucleotide comprising at least 15 nucleotides and having the particular hybridization characteristics recited in the rejected claims. Therefore, the rejected claims comprise impermissible NEW MATTER.

Further, there is no basis for the skilled artisan to predictably envision even a single oligonucleotide sequence that will meet all of the hybridization requirements recited in the rejected claims. Thus, the skilled artisan would not have been able to envision a sufficient number of embodiments to describe the claimed genus of oligonucleotides having very particular binding characteristics.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter that the applicant regards as his invention.

Claims 5, 14, 16, 18 and 23-25 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. **These are new grounds of rejection.**

Claim 5 is vague and indefinite in that the metes and bounds of the phrase "...wherein said SMRT co-repressor or peptide portion thereof is encoded by a polynucleotide having at least 80% sequence identity with SEQ ID NO: 4" are unclear. Is the polynucleotide recited in this phrase necessarily the same as the isolated polynucleotide that is being claimed or can it be a second polynucleotide (e.g. a different polynucleotide that encodes the SMRT protein, or portion thereof, and which is different from the claimed polynucleotide because of the degeneracy of the

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genetic code and/or because the two different polynucleotides comprise additional, different sequences from one another)?

Claim 14 recites a “first isolated polynucleotide encoding a SMRT co-repressor” and then recites that the first polynucleotide is selected from a Markush group of different polynucleotides. It is unclear how the nucleotides of part (d) can encode a SMRT co-repressor, or portion thereof, when they are *complementary* to sequences in parts (a)-(c) that actually do encode an SMRT co-repressor. Similarly, claim 16 also recites that the first polynucleotides of part (d) have 80% identity to the *complement* of sequences in parts (a)-(c).

Claim 23 is vague and indefinite in that the metes and bounds of the phrase “suitable stringency conditions” are unclear. The phrase is used in the context of an identified oligonucleotide comprising at least 15 nucleotides that hybridizes to a polynucleotide of claim 4, but not to a polynucleotide encoding SEQ ID NO: 11 or to a polynucleotide encoding an amino acid sequence consisting of amino acids 1031 to 2517 of SEQ ID NO: 5. The specification does not define these exact conditions and the skilled artisan has no basis to visualize what these “suitable” conditions might be.

Similarly, claim 25 specifies that the oligonucleotide of claim 23 hybridizes under “suitable stringency conditions” to a polynucleotide encoding SEQ ID NO: 5 or SEQ ID NO: 7, but does not hybridize to a polynucleotide encoding SEQ ID NO: 9.


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Conclusion

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Gerald G. Leffers Jr., PhD whose telephone number is (571) 272-0772. The examiner can normally be reached on 6:30-4:00.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Remy Yucel can be reached on (571) 272-0781. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).


Gerald G Leffers Jr., PhD
Primary Examiner
Art Unit 1636
GERRY LEFFERS
PRIMARY EXAMINER

ggl

Mon Apr 19 08:15:02 2004

us-09-522-753-5.rge

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 15, 2004, 22:23:25 ; Search time 20448 seconds

(without alignments)
5335.212 Million cell updates/sec

Title: US-09-522-753-5

Perfect score: 13215

Sequence: 1 MGSSTQLVAQTWATEPRYP.....WDBEPKPLLCQYETLSDSE 2517

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Database:

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5: gb_ov:
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9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vi:
15: gb_ba:
16: em_fun:
17: em_hum:
18: em_in:
19: em_mus:
20: em_or:
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25: em_pl:
26: em_ro:
27: em_sts:
28: em_un:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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2	12978	98.2	8636	9	AF125672	AF125672 Homo sapi
3	11067	83.7	8338	10	AF113001	AF113001 Mus muscu
4	10832	82.0	8544	10	AF125671	AF125671 Mus muscu
5	9894	74.9	7435	10	AF113002	AF113002 Mus muscu
6	7885	59.7	5339	9	HSU37146	U37146 Human silen
7	4612	34.9	2330	9	S83390	S83390 T3 receptor
8	4194	31.7	7839	9	AB028970	AB028970 Homo sapi
9	4187	31.7	7730	10	MMU35312	U35312 Mus musculu
10	4147.5	31.4	7940	6	AX578069	AX578069 Sequence
11	4147.5	31.4	7940	9	AF044209	AF044209 Homo sapi
12	4043	30.6	8038	9	AF087856	AF087856 Homo sapi
13	4009.5	30.3	8539	5	AF495886	AF495886 Xenopus l
14	3736.5	28.3	19480	2	AC139377	AC139377 Mus muscu
15	3479.5	26.3	25439	2	AC097560	AC097560 Rattus no
16	3445	26.1	21819	2	AC136560	AC136560 Rattus no
17	3344.5	25.3	21339	2	AC121005	AC121005 Rattus no
18	3178	24.0	2802	9	BC004326	BC004326 Homo sapi
19	3012	22.8	2934	10	BC047524	BC047524 Homo sapi
20	2891.5	21.9	20523	9	AC073916	AC073916 Homo sapi
21	2187	16.5	3130	9	AF303586	AF303586 Homo sapi
22	2155	16.3	1937	5	BC054296	BC054296 Xenopus l
23	2091.5	15.8	6338	10	AB093281	AB093281 Mus muscu
24	1900	14.4	6541	9	AB019524	AB019524 Homo sapi
25	1839	13.9	4235	10	MUSRIPI13	L78294 Mus musculu
26	1687	12.8	1831	9	BC050594	BC050594 Homo sapi
27	1633	12.6	1830	9	BC058511	BC058511 Homo sapi
28	1633	12.4	1731	9	BC058511	BC058511 Homo sapi
29	1628.5	12.3	3035	5	BC049302	BC049302 Danilo rer
30	1396	10.6	16190	2	AC027706	AC027706 Homo sapi
31	1391	10.5	2934	9	AK127788	AK127788 Homo sapi
32	1272	9.6	3575	9	HSN803410	HSN803410
33	1172.5	8.9	3937	9	AF303585	AF303585 Homo sapi
34	1162	8.8	13337	5	AL590153	AL590153 Zebrafish
35	1113	8.4	630	6	AX677743	AX677743 Sequence
36	1099	8.3	11236	3	AF175223	AF175223 Drosophil
37	1076	8.1	802	6	BD221548	BD221548 Human gen
38	960	7.3	525	6	AX677866	AX677866 Sequence
39	932	7.1	530	9	HSU80750	U80750 Homo sapien
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41	880	6.7	738	6	AX753058	AX753058 Sequence
42	845	6.4	730	6	BD021376	BD021376 Novel gen
43	845	6.4	730	6	BD101314	BD101314 Novel gen
44	774.5	5.9	603	6	AX677865	AX677865 Sequence
45	763.5	5.8	13531	9	AC068279	AC068279 Homo sapi
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Query Match: 100.00%
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Mismatches: 0
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US-09-522-753-5 (1-2517) X AP113003 (1-8561)

Qy	1	MetSerGlySerThrGlnLeuValIleGlnThrTrpArgAlaThrGlnProArgTyrPro	20
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Qy	21	ProHisSerLeuSerTyrProValGlnIleAlaArgThrHisTyrAspValcIyLeuLeu	40
Db	62	CCCCACAGCCTTTCTTACCCAGTGCAGATCGCCCGAAGCCACACAGGAGCTCGGGCTCTGT	121
Qy	41	GluTyrGlnHisHisSerArgAspTyrAlaSerHisLeuSerProGlyIleGln	60
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Qy	61	ProGlnArgArgProSerLeuLeuSerGluPheGlnProGlyIleAsnGluArgSerGln	80
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Qy	101	GluPheIleGluSerIleArgProArgLeuGluLeuLeuProAspProLeuLeuArgPro	120
Db	302	GAGTTCATTTGAAGAAGCGCCCTCGGTAGAGTGTGCTGTGACCCCTGTCTGCGACCG	361
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Db	362	TCACCCCTGTGTGGCCACCGGCGCAGCTGCGGGATCTGAAGACCTCACCAAGGACCGTAC	421
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Db	422	CTGACGGGCAAGTGGACCGGTGTCTCCCCCAGGCCCCCGCACACTGACCCCTGAGCTG	481
Qy	161	GluLeuValProProArgLeuSerIleGluLeuIleGlnAsnMetAspArgValAsp	180
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Qy	181	ArgGluIleThrMetValGluGlnGlnIleSerLysLeuLysLysGlnGlnGlnLeu	200
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Qy	201	GluGluGluAlaIleProGluProGluIleProValSerProProIleGlu	220
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Qy	221	SerLysHisArgSerLeuValGlnIleIleTyrAspGluAsnArgLysAlaGluAla	240
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Qy	241	AlaHisArgIleLeuGluGlyProGlnValGluLeuProLeuTyrAsnGlnPro	260
Db	722	GCACATCGAATCTGGAGGCTTGGGGCCCGAGGTGGAGCTGCCCTGTATCAACAGACCC	781
Qy	261	SerAspThrArgGlnTyrHisGluAsnIleIleGlyIleAsnGlnAlaMetArgLysLysLeu	280
Db	782	TCCGACACCCGGCAGTATCATGAGAACATCAANAATAACCGAGCGGATGCGGGAAGAAGCTA	841
Qy	281	IleLeuTyrPheLysArgAsnHisAlaArgLysGlnTrpLysGlnLysPheCysGln	300
Db	842	ATCTTGTACTTCAAGGAGGAGGATCACTCGCTCGGAACAAATGGAAGCAGAGAGTTCTGCCAG	901
Qy	301	ArgTyrAspGlnLeuMetGluAlaLeuGluLysValGluIleGluAsnAsnPro	320
Db	902	CGCTATGACCHGCTCATGAGGCTTTGGAAAAAAGGTGGAGCGCATCGAAAAACAACCCG	961
Qy	321	ArgArgAlaIleGluSerLysValArgGluTyrTyrGluLysGlnPheProGluIle	340
Db	962	CGCCGGCGGGCCCAAGGAGACGAAGTGGCGAGTACTAGAAAAGCAAGTTCCTCGAGATC	1021

Qy 701 GluAspGluMetGluAlaSerGlyValSerGlyAsnGluGluMetValGluGlu 720
Db 2102 GAGGATGAGGAGATGAGAGGCTCGGGCTGAGCGAAATGAGGAGGATGCTGAGGAG 2161
Qy 721 AlaGluAlaLeuHisAlaSerGlyAsnGluValProArgGlyGluCysSerGlyProAla 740
Db 2162 GCTGAAGCTTACATGCTCTGGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2221
Qy 741 ThrValAsnAsnSerAspThrGluSerIleProSerProHisIleThrGluAlaAlaLys 760
Db 2222 ACTGTCAACACAGCTCAGACCGAGAGCATCCCTCTCTCCACACTGAGGCGCCCAAG 2281
Qy 761 AspThrGluGlnAsnGlyProLysProAlaThrLeuGlyAlaAspGlyProPro 780
Db 2282 GACACAGGCGAGATGGGCCCAAGCCCCCAGCCCTTGGGGCGCGAGCGCCACCCCA 2341
Qy 781 GlyProThrProProArgArgThrSerArgAlaProIleGluProThrProAlaSer 800
Db 2342 GGGCCACCCACCCACACGAGAGACATCCCGGGCCCCCATTTAGAGCCCAACCCCGGCTCT 2401
Qy 801 GluAlaThrGlyAlaProThrProAlaProProAlaProProSerProSerAlaProPro 820
Db 2402 GAAGCCACCGAGGCGCTTACGCCCCCAGCCAGCACCCCTCATCGCCCTCTGCACCTCTCT 2461
Qy 821 ValValProLysGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 840
Db 2462 GTGGTCCCNAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2521
Qy 841 GluGluGlnLysProProAlaAlaGluGluLeuAlaValAspThrGlyLysAlaGluGlu 860
Db 2522 GAGGAGCAAGAGCCCGCGCGCTGAGGAGCTGGCAGTGGACACAGGAGAGCGCGAGGAG 2581
Qy 861 ProValLysSerGluCysThrGluGluAlaGluGluGluGluGluGluGluGluGlu 880
Db 2582 CCGCTCAAGAGCGAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2641
Qy 881 GluAlaAlaGluAlaThrAlaGluGluAlaLeuLysAlaGluLysLysGluGlySer 900
Db 2642 GAGCGCGCTGAGGCGACCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2701
Qy 901 GlyArgAlaThrAlaLysSerSerGlyAlaProGlnAspSerAspSerSerAlaThr 920
Db 2702 GGAGGCGCCACCATGCGCAAGAGCTCGGGCGCCCCCAGGACAGGACATCCAGTCTACC 2761
Qy 921 CysSerAlaAspGluValAspGluAlaGluGlyGlyAspLysAsnArgLeuLeuSerPro 940
Db 2762 TGCAGTGCAGACGAGGTGGATGAGGCGGAGGCGGCGGACAGAACCGGTGTGTCCCA 2821
Qy 941 ArgProSerLeuLeuThrProThrGlyAspProArgAlaAlaSerProGlnLysPro 960
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Qy 961 LeuAspLeuLysGlnLeuLysGlnArgAlaAlaAlaIleProIleGlnValThrLys 980
Db 2882 CTGGACCTGAAGACAGCTGAAGACGAGCGGCTGCGCATCCCGCCCATCCAGGTCAACAA 2941
Qy 981 ValHisGluProProArgGluAspAlaAlaProThrLysProAlaProProAlaProPro 1000
Db 2942 GTCCATGAGCCCCCGGAGGAGCGAGCTCCCAAGCCAGCTCCCGCCAGCCCGCCAG 3001
Qy 1001 ProProGlnAsnLeuGlnProGluSerAspAlaProGlnGlnProGlySerSerProArg 1020
Db 3002 CCACCGCAAAACCTTGACGCGGAGAGCGAGCGCTCTCAGCAGCTGGCAGGAGCCCCCG 3061
Qy 1021 GlyLysSerArgSerProAlaProProAlaAspLysGluAlaPheAlaAlaGluAlaGln 1040
Db 3062 GGCAAGAGCAGGAGCGCGCACCCCGCGGACAGAGGAGGCTTCGACGCGGAGGCCAG 3121
Qy 1041 LysLeuProGluValProProCysThrThrSerGlyLeuProPheProValProArg 1060
Db 3122 AAGCTGCTGGGAGCCCCCTTGTGAGCTTCCGGGCTGCGCTTCCCGGCTGCGCCCGT 3181
Qy 1061 GluValLysAlaSerProHisAlaProAspProSerAlaPheSerThrAlaProPro 1080

Db 3182 GAGGTGATCAAGGCTCTCCCGCATGCCCGAGCCCTCAGCCCTTCTCTACGCTCCACCT 3241
Qy 1081 GlyHisProLysProLysLeuHisAspThrAlaAspProValLeuProAspProPro 1100
Db 3242 GGTCAACCACTGCTCCCTGGGCTCATGACACTGCCCGGCGCTCTGCCGCGCCACCC 3301
Qy 1101 ThrLysSerAspProProProLysLeuHisSerSerAlaLysHisProSerValLeuGluArg 1120
Db 3302 ACCATCTCAACCGCGCTCCCTCATCTCTGCGCAAGCACCCCGAGGCTCTCGAGAG 3361
Qy 1121 GlnIleGlyAlaIleSerGlnGlyMetSerValGlnLeuHisValProLysSerGluHis 1140
Db 3362 CAATAGGTGCATCTCTCCCAAGGAATGTGGTCCAGCTCCAGCTCCGCTACTCAGAGCAT 3421
Qy 1141 AlaLysAlaProValGlyProValThrMetGlyLeuProLeuProMetAspProLysLys 1160
Db 3422 GCCAAGCCCGCTGGGCTCTGTCCATTTGGGCTGCTCCCTGCTCATGAGCCCAAGAG 3481
Qy 1161 LeuAlaProPheSerGlyValLysGlnGluLeuSerProArgGlyGlnAlaGlyPro 1180
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Qy 1241 GlyThrIleThrArgIleGlyGluAspSerProSerArgLeuAspArgGlyArgGlu 1260
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Qy 1261 AspSerLeuProLysGlyHisValIleThrGlyLysGlyHisValLeuSerThr 1280
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Db 4022 AGCCCCCAGCATCTCAAGAGCAGCACCATCCGCGGTCCATCACCAAGGAGATCCCT 4081
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Db 4322 CTGGCGCGCGCGCTCAAGGAGGCTCCATCAGCGAGGACACCGCGCTCAAGTACGAC 4381
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Qy 1501 ArgAlaCysTyrGluGluSerLeuLysSerArgProGlyThrAlaSerSerGlyGly 1520
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Qy 1521 SerIleAlaArgGlyAlaProValIleValProGluLeuGlyLysProArgGlaSerPro 1540
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Qy 1541 LeuThrTyrGluAspHisGlyAlaProPheAlaGlyHisLeuProArgGlySerProVal 1560
Db 4622 CTGACCTATGAGGACACCGCGGCGACCTTTTGCAGGCGCACCTCCACGAGGTTGCGCGTG 4681
Qy 1561 ThrMetArgGluProThrProArgLeuGlnGlySerLeuSerSerSerIleAlaSer 1580
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Qy 1581 GlnAspArgLysLeuThrSerThrProArgGluIleAlaLysSerProHisSerThrVal 1600
Db 4742 CAGGACCGAAGCTGACGTGACGCTGTGATGATGCGCAAGTCCCGCGCACGACCGCTG 4801
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Qy 1701 ThrAlaMetAlaGlnArgAlaAspMetLeuArgGlyLeuSerProArgGluSerSerLeu 1720
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Db 5222 CTGTGCTGTGGCGCGCGACACCGAGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5281
Qy 1761 LeuProThrAlaProGlnProPheSerSerArgHisSerSerSerProLeuSerProGly 1780
Db 5282 CTCCCGACCG 5341
Qy 1781 GlyProThrHisLeuThrLysProThrThrThrSerSerSerGluArgGluArgAspArg 1800
Db 5342 GGTCCACACACTTTCACAAACCCACCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5401

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Qy 1821 ValGluHisAlaProIleThrArgProGlyThrGluGlnSerSerGlySerSerGlySer 1840
Db 5462 GTGGAGCAGCGCGCGCGCTCGAGACTGTGTACAGAGCAGCAGCAGCAGCAGCAGCAGC 5521
Qy 1841 SerGlyGlyGlyGlyGlySerSerSerArgProAlaSerHisSerHisAlaHisGlnHis 1860
Db 5522 AGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 5581
Qy 1861 SerProIleSerProArgThrGlnAspAlaLeuGlnGlnArgProSerValLeuHisAsn 1880
Db 5582 TCGCCCATCTCTCGCGACCCAGGATGCCCTCCAGCAGCAGCAGCAGCAGCAGCAGCAGC 5641
Qy 1881 ThrGlyMetLysGlyIleIleThrAlaValGluProSerLysProThrValLeuArgSer 1900
Db 5642 ACAGGCGTGAAGGATATCATCGCTGTGGAGCCAGCAGCAGCAGCAGCAGCAGCAGCAG 5701
Qy 1901 ThrSerThrSerSerProValArgProAlaAlaThrPheProProAlaThrHisCysPro 1920
Db 5702 ACCTCCACCTCTCCACCGCTTCCCGAGCTGCCATCTCCACCTGCCACCTGCCAC 5761
Qy 1921 LeuGlyGlyThrLeuAspGlyValTyrProThrLeuMetGluProValLeuLeuProLys 1940
Db 5762 CTGGCGGCGCACCTCGATGGGCTTACCCTACCTCATGGAGCCGCTTGTCTGCCAAG 5821
Qy 1941 GluAlaProArgValAlaAlaArgProGluArgProArgAlaAspThrGlyHisAlaPheLeu 1960
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Db 5882 GCCAAGCGCGCGCGCGCGCTCGGCTGAGCGCGCGCTCTCTCCCGCAGCAGGCGCTGGAG 5941
Qy 1981 ProArgProLeuValProValSerGlyHisAlaThrIleAlaArgThrProAlaLys 2000
Db 5942 CCGCGCGCGCTTGTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6001
Qy 2001 AsnLeuAlaProHisHisAlaSerProArgProAlaProProAlaSerAlaSerAsp 2020
Db 6002 ARCTCGACCTTACACCG 6061
Qy 2021 ProHisArgGlyLysThrGlnSerLysProPheSerIleGlnGluLeuGluLeuArgSer 2040
Db 6062 CCGCACCGCGGAAAGAGCTCAAGTAAACCTTTTCCATCCAGGAACTGGAACTCCGTTCT 6121
Qy 2041 LeuGlyTyrHisGlySerSerTyrSerProGluGlyValGluProValSerProValSer 2060
Db 6122 CTGGGTATCCAGCGCAGCAGCTACAGCCCGGAGGGGTGGAGCCCTCGAGCTCTGTGAGC 6181
Qy 2061 SerProSerLeuThrHisAspLysGlyLeuProLysHisLeuGluLeuLeuAspLysSer 2080
Db 6182 TCACCCAGTCTACCCACGCAAGGGGCTCCCGCAGCAGCAGCTGGAGAGCTCGCAGAGAGC 6241
Qy 2081 HisLeuGluGlyLeuLeuArgProLysGlnProGlyProValLysLeuGlyGlyGluAla 2100
Db 6242 CACCTGGAGGGGAGCTGCGGCGCAAGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCG 6301
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Qy 2121 GlnThrAlaProGlyValLysGlyHisGlnArgValValThrLeuAlaGlnHisSer 2140
Db 6362 CAGACCG 6421
Qy 2141 GluValIleThrGlnAspTyrThrArgHisHisProGlnGlnLeuSerAlaProLeuPro 2160
Db 6422 GAGGTCTATCAGCAGGACTACACCGCGCACCCAGCAGCAGCTCAGCGCGCGCGCGCGCG 6481

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PAITGCTMYASOAVOEHASTNMLEAIIKXALGKXDORHESPRISANAPNLELNS
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LAGPHHAWDEBPFLKCSQYETLSDSE"

ORIGIN

Alignment Scores:

Pred. No.: 1,26e-254 Length: 8686
Score: 12978.00 Matches: 2487
Percent Similarity: 98.57% Conservative: 3
Best Local Similarity: 98.46% Mismatches: 9
Query Match: 98.21% Indels: 28
DB: 3 Gaps: 3

US-09-522-753-5 (1-2517) x AF125672 (1-8686)

Qy 1 MetSerGlySerThrGlnLeuValAlaGlnThrTrpArgAlaThrGluProArgTyrPro 20
Db 157 ATGTGCGGCTCCACACAGCCTGTGGCACAGCTGTGGAGGCCACTGAGCCCGCTACCCG 216
Qy 21 ProHisSerLeuSerTyrProValGlnIleAlaArgThrHisThrAspValGlyLeuLeu 40
Db 217 CCCACAGCCTTCTTACCCACAGTCAGATCCCGCGGACGACACAGGAGTGGGCTCTG 276
Qy 41 GluTyrGlnHisHisSerArgAspTyrAlaSerHisLeuSerProGlySerIleIleGln 60
Db 277 GAGTACACAGCACCCTCCCGGACTATGCTCCACCTGTCGCGCGGCTCCATCATCCAG 336
Qy 61 ProGlnArgArgProSerLeuLeuSerGluPheGlnProGlyValAsnGluArgSerGln 80
Db 337 CCCACAGCGGAGGCCCTCCCTGCTGTGAGTTCACGCGCGGGAATGAACGGTCCAG 396
Qy 81 GluLeuHisLeuArgProGlnSerHisSerTyrLeuProGluLeuGlyLeuSerGluMet 100
Db 397 GAGCTCCACTGCGGCCAGAGTCCCACTCATCTGCTCCGAGGCTGGGAGTCAAGATG 456
Qy 101 GluPheIleGluSerIysArgProArgLeuGluLeuLeuProAspProLeuLeuArgPro 120
Db 457 GAGTTCATTTGAAGCAAGCGCCCTCGGCTAGAGCTGTGCTGACCCCTCTGTCGACCG 516
Qy 121 SerProLeuLeuAlaThrGlyGlnProAlaGlySerGluAspLeuThrIysAspArgSer 140
Db 517 TCACCCCTGCTGGCCACAGGCGGCTGCGGGATCTGAAGACCTCACCAAGACCGTAGC 576
Qy 141 LeuThrGlyIysLeuGluProValSerProSerProSerProSerProHisThrAspProGluLeu 160
Db 577 CTGAGGGCAAGCTGGAGAACCGGTGTCTCCCCAGGCCCGCCGACACTGACCTGAGCTG 636
Qy 161 GluLeuValProProArgLeuSerIysGluLeuLeuIleGlnAsnMetAspArgValAsp 180
Db 637 GAGCTGTGTGCGCCACCGCTGTCCAAGGAGGAGCTGATCCAGAAATGAGACCGGTGAC 696
Qy 181 ArgGluIleThrMetValGlnGlnIleSerIysLeuLeuValIysGlnIleGlnIleLeu 200
Db 697 CGAGAGATCACCATTGAGCAGCAGATCTTAAGCTGAGAGAGAGAGAGAGAGAGAGAG 756
Qy 201 GluGluAlaAlaIysProProGluProGluIysProValSerProProProIleGlu 220
Db 757 GAGGAGGAGGCTGCAAGCGCGCGGAGGCTGAGAAGCGCGGTGTCACCCCGCCCATCGAG 816
Qy 221 SerIysHisArgSerLeuValGlnIleIleTyrAspGluAsnArgIysLeuAlaGluAla 240
Db 817 TCGAAGCACCGCAGCCTGTGTGAGATCATCTACGACGAGAACCGGAGAGGCTGAAGCT 876
Qy 241 AlaHisArgIleLeuGlyLeuGlyProGlnValGluLeuProLeuTyrAsnGlnPro 260

Db 877 GCACATCGGATCTCTGGAAGAGCCCTGGGCGCCCGAGGTGGAGCTGTCGTACACACGAGCC 936
Qy 261 SerAspThrArgGlnTyrHisGluAenIleLysIleAenGlnAlaMetArgIysIysLeu 280
Db 937 TCCGACACCCCGGACGATCATGAGAACATCAAAAATAAACACGAGCGATGCGGAGAGACTA 996
Qy 281 IleLeuTyrPheIysArgArgAenHisAlaIleGlyGlnTyrIleGlyLeuIysPheCysGln 300
Db 997 ATCTTGACTTTCAGAGAGAGATCATCGCTCGAANAACANTGGAGCAGAGATTTCTGCCAG 1056
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Db 1057 CGCTATGACCACTCATGAGAGCCCTGGGAGAGAGAGGTGGAGCGCATCGAGAGAACACCC 1116
Qy 321 ArgArgArgAlaIysGluSerIysValArgGluTyrTyrGluIysGlnPheProGluIle 340
Db 1117 CGCGCGCGCGGACGAGGAGACCAAGTTTCGCGAGTACTACGAGAGACGATTTCCCTGAGATC 1176
Qy 341 ArgIysGlnArgGluLeuGlnArgMetGlnSerArgValGlyGlnArgGlySerGly 360
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Db 1294 GACACAGAGAGCTGGAGAGACAGATGCGCCAGCTGGCGGTGATCCCGCCCATCTGTGTAC 1353
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Db 1354 GAGCTGACACACAGCGCATCAAGTTTCATCAACATGAACCGGCTTATGCGCGACCCCATG 1413
Qy 421 LysValTyrLysAspArgGlnValMetAsnMetTrpSerGluGlnGluIysGluThrPhe 440
Db 1414 AAGGTGTACAAATGACCCCGCAGGTCATGAACATGTGTGAGTGAGCAGGAGAGAGACCTTC 1473
Qy 441 ArgGluIysPheMetGlnHisProLysAsnPheGlyLeuIleAlaSerPheLeuGluArg 460
Db 1474 CGGAGAGATTCATGACAGCATCCCAAGACTTTGSCCTGATCGCATCATCTCTGTGAGAG 1533
Qy 461 LysThrValAlaGluCysValLeuTyrTyrTyrLeuThrIysIysAenGluAenTyrIys 480
Db 1534 AAGACAGTGGCTGAGTGGCTCTTATTAATCTACTGACTAAGAGAAATGAGAACTATTAAG 1593
Qy 481 SerLeuValArgArgSerTyrArgArgGlyIysSerGlnGlnGlnGlnGlnGln 500
Db 1594 AGCCTGCTGAGATCGAGCTATCGCGCGCGCAGAGACCATCTCAGGGGAGGACCAACAGCAG 1653
Qy 501 GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 520
Db 1654 CACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1713
Qy 521 AspGluIysGluIysGluIysGluIysGluIysGluIysGluIysGluIysGluIys 540
Db 1714 GATGAGAGGAG 1773
Qy 541 AspLysGluAsnLeuLeuLysThrAspAspThrSerGlyGluAspAsnAspGlu 560
Db 1774 GACACAGAGAGACTCTCTCAAGGAGAGAGACAGACGACACCTCAGGGGAGGACCAACAGCAG 1833
Qy 561 LysGluAlaValAlaSerIysGlyArgIysThrAlaAenSerGlnIysArgIysGly 580
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Qy 581 ArgIleThrArgSerMetAlaAenGluAlaAenSerGluIleAlaIleThrProGlnGln 600
Db 1894 CGCATCACCCGCTCAATGGCTTAATGAGGCCAACAGGAGGAGGCGCATCAACCCCGCAGCAG 1953
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Db 1954 AGCCCGAGCTGGCTCCATGGAGCTGAATGAGAGTTCTCGTGGACAGAGAGAAATG 2013
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Db 2014 GAACAGCCCAAGAGGTCTCTGGACACGCGCCCACTGGTGGCCATCGCCGGATG 2073
Qy 641 ValGlySerIleThrValSerGlnCysLysAsnPheTyrPheAsnTyrIleLysArgGln 660
Db 2074 GTGGGTCCAGACTGTGTGCGAGTGAAGACTTCTACTTCACTACAGAGAGAGGCG 2133
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Db 2134 AACCTCGATGAGACTTTCAGACAGCAAGCTGAAGATGGAGAGAGAGAAACGCGCG 2193
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Qy 701 GluAspGluGluMetGluAlaSerGlyValSerGlyAsnGluGluGluMetValGluGlu 720
Db 2254 GAGGATGAGGAGATGGAGGCGTGGCGGTGACGGGAAATGAGAGGAGATGGTGGAGAG 2313
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Db 2314 GCTGAA-----GCC 2322
Qy 741 ThrValAsnAsnSerSerAspThrGluSerIleProSerProHisThrGluAlaLys 760
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Qy 761 AspThrGlyGlnAsnGlyProLysProAlaThrLeuGlyAlaAspGlyProPro 780
Db 2383 GACACAGGGCAATGGCGCCCAAGCCCGCAGCCACCTCGCGCGCGAGCGGCCCA 2442
Qy 781 GlyProProThrProPro-ArgArgThrSerArgAlaProIleGluProThrProAla 800
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Db 2502 TGAAGCCACTTAGCCCTTAGCCCTCAGCCCGCCAGAGACCCCATTTCTTCACTTCTCC 2561
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Db 2682 GCCCGTCAAGAGGAGTGCAGGAGGAGCCGAGGAGGCGCGCCAGGCGAGGAGCGC 2741
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Db 2742 GGAGGCGCTGAGGCGCAGCGCGAGAGGCGCTCAAGGACAGAGAGAGGAGGCGGG 2801
Qy 900 rGlyArgAlaThrThrAlaLysSerGlyAlaProGlnAspSerAspSerAlaThr 920
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 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 8544)
 Park, E. J., Schreen, D. J., Yang, M., Li, H., Li, L. and Chen, J. D.
 SMRte, a silencing mediator for retinoid and thyroid hormone
 receptors-extended isoform that is more related to the nuclear
 receptor corepressor
 Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3519-3524 (1999)
 MEDLINE 99199215
 PUBMED 10097068
 REFERENCE 2 (bases 1 to 8544)
 Chen, J. D.
 Direct Submission
 TITLE Submitted (03 FEB-1999) Pharmacology and Molecular Toxicology,
 University of Massachusetts Medical School, 55 Lake Avenue North,
 Worcester, MA 01655, USA
 FEATURES Location/Qualifiers

source

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PPIVTKHEPREDTVPKPPVPPPTQHLQPEGDVSOQSGSPGKSRSPVPAEK
BAEPAPFPAPTEGQSLPHAGHLPSHPREVIKTSTRADPLFSYTPPGHPLP
GLHDSAPVLPRPISNPPPLISSAKHPGLERQLAGISQMSVQLRVPHSHEKPMG
PLTMELAVDPKKGALTALAPPVPEASQVPCRRPQLQRLYHPTPADVLVYKGT
ISRVGSDSPSLRDAREDTLPKGVIEYEGKHVLSYEGGVSQSGSKEDSSSGP
PHEATAKRYDMMGRVGRVTSATSEGLMGRAIPROHSPLKXOHHIRGSTGQIP
RSVYAEQDYLREKAKLRKRGTPPPPPRDLTETYPKPLDPLGLKLPKTHGV
ATVKEAGSIHEIPRELRPELPAPRLPKEGSITQGTPLKYDSCAPSTGKHDV
RSIIGSGRFPFALHDLIMADALACRACESLSKSGSTSGAGSGSITRGAPVVP
ELGPROSPUTYEDHGAFTSHLSPGSPVITREPTPLQSGSLSSKASQDKLSTP
REIASKPSHTVPEHHPFISPEHLKRGVTVGLVYHGHIPLAFTSIPRIGLEAA.
AAVTLPHLAPSPHYLLPYLYGYDPTAALNNQTIINDYITSQOMHNAAMA
QADMLRGLSPRESSALNYSAGPRGIDLSQVPHLPVLPPTPTPTAIDRLA
TAPPPSRHSSPLSPGCPHAKPTATSSERERERERERERERERERERERER
WRPTEQSGAGSGSRPASHTHQSPISPTQDALQQRPSVLNHTSMKGVTSVFGT
PTVLRSSTSSVVRPAATFPFATHCPGLGTLEGVPTLMEPVLKPETSVAPRPPR
VDGHAFTKPPAPRSPASSPKSSEPSLAPSSSHTAIRTAKSLAPHASPPDPG
PTASDLHREKTKSPFSIOELRSLSYHSGAGYSPDQVPIPSVSPSLTHDKGLS
KPLBEKSLHGLERHKGPGPKMSAEAAHLPHRLPSPESQSSPLLOTAPGLKH
QVUTVLAQHSLEVTQDTRHHPQOLSGPLPABLSFGASCPVLDLRLPPSDVLP
PDHGTARGSPHSGGKSPSPKISVILGSSSEDAIEPVSPEGMTEPHCARAVPFL
YRQGEGRPMGSGFNTSQPAPFSLKTSNSAWKSKQKQKGLNTHNRNPP
NIGQGFIEFNPAITAGMLTCKSQVQEHASTNGLLEAIRKALMGKDYDQEP
LGNAPFLNANASAPAAEMPTTADGSDHAUTSPGGKAKVSGSPSRKAKSP
GLASGDRPSPSVSGSDGDCNRFTLNRYWEDRPSAGSTPPFPYPLNRLQAGVMA
SPPPPLAAGSGPLAGPHAWDEBPKEPLLCQVETLSDSE"

ORIGIN

Alignment Scores:

Pred. No.: 3,11e-211 Length: 8544
Score: 1082.50 Matches: 2149
Percent Similarity: 87.94% Conservative: 90
Best Local Similarity: 84.41% Mismatches: 197
Query Match: 81.97% Indels: 117
DB: 10 Gaps: 33

US-09-522-753-5 (1-2517) x AF125671 (1-8544)

Qy 1 MetSerGlySerThrGlnLeuValAlaGlnThrTyrArgAlaThrGluProArgTyrPro 20
Db 160 ATGTCCAGGATCCACACAGCTGTGGCAGACATGCGGGCTGCTGAGCCCCCGCTACCCA 219

Qy 21 ProHisSerLeuSerTyrProValGlnIleAlaAargThrHisThrAspValGlyLeuLeu 40
Db 220 CCCCATGGCATCTCTTACCCTGGGTGAGATAGCCCGGTCCACACGAGCGTGGGGCTGCTT 279
Qy 41 GluTyrGlnHisHisSerArgAargTyrAlaSerHisLeuSerProGlySerIleIleGln 60
Db 280 GAGTACCAACACACCCCGGTGACTAACCTCACACCTGTCCACCGGTTCATCATCCAG 339
Qy 61 ProGlnArgAargTyrProSerLeuLeuSerGluPheGlnProGlyAengluAargSerGln 80
Db 340 CCACAGAGGAGTGGCCCTCTCACTGTGTCTCAGAGTTCACAGCTGGGAGTGAAGCGTTCAG 399
Qy 81 GluLeuHisLeuArgProGluSerHisSerTyrLeuProGluLeuGlyLysSerGluMet 100
Db 400 GAGCTCCACCTGCGCCCTGAGTCCCGCAGCTTCTCTGCTGAGCTGGGCAAGCCGACATA 459
Qy 101 GluPheIleGluSerLysArgAargProArgLeuGluLeuLeuProAspProLeuLeuArgPro 120
Db 460 GAATTCACCGAGCGCAAGCGCCCGCCCTGGAGCTACTACCCGATACCTCTGCTGGCCCA 519
Qy 121 SerProLeuLeuIleThrGlyGlnProAlaGlySerGluAspLeuThrLysAspArgSer 140
Db 520 TCACCCCTGCTGCCACTGGGGCAGCGAGTGGGTCTGAAGACCTTACCAAGGACCGGTAGC 579
Qy 141 LeuThrGlyLysLeuGluProValSerProProSerProProHisThrAspProGluLeu 160
Db 580 CTGGCAGGCACTGGAGCGCTGTGTCACTCCCTCAGTCCCGCGCAGCTGACCTGAGCTA 639
Qy 161 GluLeuValProArgLeuSerLysGluLeuLeuIleGlnAen--MetAspArgVal 179
Db 640 GAGCTGGCCCATCTCCACTGTCTCAAGGAGGAGCTGATCCAGAACAGATTCAGACCGCGTG 699
Qy 180 AspArgGluIleThrMetValGluGlnGlnIleSerLysLeuLysLysGlnGlnGln 199
Db 700 GACCGTGTAGATGCATCATGTGTAGCAGCAGCAGATCTCAAGCTGAAGAGAAGCAGCAACAG 759
Qy 200 LeuGluGluGluAlaAlaLysProGluProGluLysProValSerProProIle 219
Db 760 TTGGAGGAGGAGCCCGCCAAAGCCCGCGAAGCGCTGTGTGCGCACCCACCCATA 819
Qy 220 GluSerLysHisArgSerLeuValGlnIleLysLeuLeuAenArgLysLysLysLys 239
Db 820 GAATCAAGACATGAAGCCCTGGTCCAGATCATCTACGATGAGAACCGGAGAAAGCCGAA 879
Qy 240 AlaAlaHisArgIleLeuGluGlyLeuGlyProGlnValGluLeuProLeuTyrAenGln 259
Db 880 GCGGCACACCGGCTCTCTAGAACGCTGGGGGCCCCAGGTGGAGCTGCTCTGTACAACACAG 939
Qy 260 ProSerAspThrArgGlnTyrHisGluAenIleLysLysLysLysLysLysLysLys 279
Db 940 CCGTCTGACACACCCAGTACCATGAAACATCAAAATATACCCAGGCGATGCGGAAGAG 999
Qy 280 LeuLeuLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 299
Db 1000 CTGATCTGTACTTTAAGCGGAGAAACACCGCGCGAAGCAGTGGGAGCAGCGCTTCTGCG 1059
Qy 300 GlnArgTyrAspGlnLeuMetGluAlaLeuGluLysLysValGluAargIleGluAenAen 319
Db 1060 CAGCGCTATGACTAGCTCATGAGGCGGTGGGAGAGAGGTAGAGGCGCATAGAGAACCAAT 1119
Qy 320 ProArgArgArgAlaLysGluSerLysValArgGluTyrTyrGluLysGlnPheProGlu 339
Db 1120 CCGCGNAGGAGGCCCAAGGAGAGCAAGGTGAGGGAGTACTACCGAAGAAACAGTTCCTCGGAG 1179
Qy 340 IleArgLysGlnArgGluLeuGlnGlnArgMetGlnSerArgValGlyGlnArgGlySer 359
Db 1180 ATCCGAGAGCAGTGGGAGCTGACAGGAGCGCATGACAGAGCGGTGGCGCGCTGGCGAGT 1239
Qy 360 GlyLeuSerMetSerAlaAlaArgSerGluHisGluValSerGluIleIleAspGlyLeu 379
Db 1240 GGGCTCTCCATCGGGCTGCCCGCCAGTGAAGCATGAGGTGTTCTGAGATCATATTGATGGCTG 1299

QY 380 SerGluGlnGluAenLeuGluLysGlnMetArgGlnLeuAlaValIleProProMetLeu 399
Db 1300 TCTGAGCAGGAACTTGGAGAGCAGATGCGCCAGCTGCGCGATCC - GCCATGTG 1357
QY 400 TyrAspAlaAspGlnGlnArgIleLysPheIleAenMetAenGlyLeuMetAlaAspPro 419
Db 1358 TAGCAGCC - GACCAGCAGAGANTCAAGTTTCATCAATGATGATCTCATGATGACCCC 1416
QY 420 MetLysValTyrLysAspArgGlnValMetAenMetTyrSerGluGlnGluLysGluThr 439
Db 1417 ATGAAGGTCTACAGGACCGTCAGGTTACCAACATGTGGAGCAGCAGGAGGACACC 1476
QY 440 PheArgGluLysPheMetGlnHisProLysAenPheGlyLeuIleAlaSerPheLeuGlu 459
Db 1477 TTCGGTGGAGAGTTTATGACAGCACCTTAGAACCTTTGGCTGATTGCTTCATCTCGAG 1536
QY 460 ArgLysThrValAlaGluCysValLeuTyrTyrLeuThrLysLysAenGluAenTyr 479
Db 1537 AGAAGACGGTCGCTGAGTGTCTTATTACTACCTGACCAAGAGAGATGAATATAC 1596
QY 480 LysSerLeuValArgSerTyrArgArgGlyLysSerGlnGlnGlnGln 499
Db 1597 AAGAGCTTGTGGCGGAGCTATCGCGCGTGGCAAGAGCCAGCAGCAGCAGCAGCAG 1656
QY 500 GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 519
Db 1657 CAAACACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1704
QY 520 LysAspGluLysGluLysGluLysGluLysGluLysGluLysGluLysGluLysGlu 539
Db 1705 AAGGAGGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1764
QY 540 AsnAspLysGluAspLeuLeuLysGluLysThrAspAspThrSerGlyGluAsnAsp 559
Db 1765 AACGAGAGGAGAGACTCAGCAAGGAGAGAGACAGACGACACTTCTGGCGAGACAGCAT 1824
QY 560 GluLysGluAlaValAlaSerLysGlyArgLysThrAlaAenSerGlnGlyArgArgLys 579
Db 1825 GAGAAAGAGCGCTGGCTCCAAAGCCGCAAACTGCCAACAGCCAGCCGCGCAGA 1884
QY 580 GlyArgIleThrArgSerMetAlaAenGluAlaAenSerGluGluAlaIleThrProGln 599
Db 1885 GGCCTATCAGCGCTCCATGGCCACGAGGCCAACCATGAGGAGACACCCACCCACAG 1944
QY 600 GlnSerAlaGluLeuAlaSerMetGluLeuAenGluSerArgTyrThrGluGluGlu 619
Db 1945 CAAAGTTGAGAGCTGGCTTCCATGAGATGAAACGAGAGTTCTCGCTGGACTGAGAGAG 2004
QY 620 MetGluThrAlaLysLysGlyLeuLeuGluHisGlyArgAenTyrSerAlaIleAlaArg 639
Db 2005 ATGGACACGCAAGAAAGCGCTCTGGAAACATGGAGGAACTGTTCAGCCATGTCGCCG 2064
QY 640 MetValGlySerLysThrValSerGlnCysLysAenPheTyrPheAenTyrLysLysArg 659
Db 2065 ATGGTGGGCTCCAGACCGTGTCCAGTGTAAAGACTTCTACTTCAACTACAGAGAGG 2124
QY 660 GlnAenLeuAspGluIleLeuGlnGlnHisLysLysLysMetGluLysGluArgAenAla 679
Db 2125 CAGAACTTGGACGAATCTTCAGCAGCACAGCTAAGATGAGAGAGGAGAGAGAGCT 2184
QY 680 ArgArgLysLysLysAlaProAlaAlaIleSerGluGluAlaIlePheProVal 699
Db 2185 CGAG 2244
QY 700 ValGluAspGluMetGluAlaSerGlyValSerGlyAenGluGluMetValGlu 719
Db 2245 GCTGAGCAGAGAGATGAGAGATCAGCGCAGCATCAGCGCAGTCCCAATGAGAGAGAGTGGCGAG 2304
QY 720 GluAlaGluAlaLeuHisAlaSerGlyAenGluValProArg - - GlyLysCysSerGly 738
Db 2305 GAGGACAGAGCTTCAGGCTCTGGGATGAGTTCCAGAGTTGGGAGTGGAGTGGAGTGG 2364
QY 739 ProAlaThrValAenAenSerSerAspThrGluSerIleProSerProHisThrGluAla 758

Db 2365 CCAGCTGCTGTCTACACAGCTCTGTACTAGAGTGTCCATCCCGCTTCAGAGCC 2424
QY 759 AlaLysAspThrLysGlnAenGlyProLysProAlaIleThr - - - - - LeuGlyAlaAep 776
Db 2425 ACGAGAGACT - - - - - GGGCTTAACCCACTGCACTGAAGCATTTGCCGCTGCC 2475
QY 777 GlyProProProLysProProThrProProArgArgThrSerArgAlaIleGluPro 796
Db 2476 ACCAGCCACTTTCCT - - - - - CCTCAGAGAAACCGCAGCAGCCCTGCTGAGCCC 2529
QY 797 ThrProAlaSerGluAlaThrGlyAlaProThrProProAlaIleProProSerProSer 816
Db 2530 TCCCGAGTCCCTATGCCAGTGGCCACCATCCAGAGCCTTCC - - - - - CCATCAGCTGCC 2586
QY 817 AlaProProProValProLysGluLysGluGluThrAlaAlaAlaProPro 836
Db 2587 GCACCCCGGCTCTGTGGACAGGATGACCAAGAGCCCGGCTGCTCCAGCTCCCGAG 2646
QY 837 ValGluGluGlyLysGluGlnLysProProAlaIleGluLysLysAlaValAspThrGly 856
Db 2647 ACAGAGATGCCAGGAGCAGAACTCTGAGGCCGAGGAG - - - - - ATCGATGTGGGA 2697
QY 857 LysAlaGluGluPro - - - - - ValLysSerGluCysThr 867
Db 2698 AAGCAGAGGAGCTCCGAGGCTCTGAGAGCCCGGAGAGTGTAAAGAGTGACCAAG 2757
QY 868 GluGluAlaGluGlyProAla - - - - - LysGlyLysAenAlaGluAlaIleAlaThr 886
Db 2758 GAGGAGCCGAGAGAGCTGAGCAAAAGCCAGGCGCAGAGGCCATTGAACTGTG 2817
QY 887 AlaGluGlyAlaLeuLysAlaGluLysGlyGlySerGlyArgAlaThr - - - - - 905
Db 2818 TCTGAGGCCACTTAAAGTGGAG - - - - - GAGGCTGTGACAGGCGAGCTGTGACCAAG 2871
QY 906 AlaLysSerSerGlyAlaProGlnAspSerAspSerAlaThrCysSerAlaAspGlu 925
Db 2872 GGTTCCAGCTCAGTGTGCCACAGGACAGTACTCCAGTCCACTGCAGTCCGATGAG 2931
QY 926 ValAspGluAlaGluGlyLysAenArgLeuLeuSerProArgProSerLeuLeu 945
Db 2932 GTGAGCAACCCAGAGAGGTGACAGGCGAGCTGTCTGTCACAGGCCCGACCTCTC 2991
QY 946 ThrProThrGlyAspProArgAlaAenAlaSerProGlnLysProLeuAenLysGln 965
Db 2992 ACCCGGCTGGAGATCCCGGCGCAGTACTCGCCCGCAGAGCCGCTGGACCTGAAGCAG 3051
QY 966 LeuLysGlnArgAlaAlaIleProProIleGlnValThrLysValHisGluProPro 985
Db 3052 CTGAGCAGGAGCAGCGCCCATCCCTATC - - - - - GTCACCAAGTCCATGAGCCGCC 3108
QY 986 ArgGluAspAlaAlaProThrLysProAlaProProAlaProProProGlnAenLeu 1005
Db 3109 CGGAGAGACACTTACCCCAAGCAGTTCCTGCTCCACCAAGCCGCTGAGACCTTA 3168
QY 1006 GlnProGluSerAspAlaProGlnGlnProGlySerSerProArgGlyLysSerArgSer 1025
Db 3169 CAGCAGAGGCTGAGCTCTCAGCAGTGGGAGGAGTCCACGTGGCAAGTCCCGCAGC 3228
QY 1026 ProAlaProProAlaAspLysGlu - - - - - AlaPheAlaAla 1037
Db 3229 CCAGTGCCTCTCCGAGAAAGGCGCAGAGAACCCGCTTCTTCCGGCTTCCCAACT 3288
QY 1038 GluAlaGlnLysLeuProGlyAspProProCysTyrThrSerGlyLeuProPheProVal 1057
Db 3289 GAGGGCCA - AAGCTTACCAGTGGAGCCCGCAGCTGCTCATCGGT - - - - - GCTTTCCTAT - - - - - 3342
QY 1058 ProProArgGluValIleLysAlaSerProHisAlaProAspProSerAlaPheSerTyr 1077
Db 3343 CTTCCAGGAGCTGATCAAGACTTCCACACGCGCT - - - - - GACCT - - - - - CTCTTCTCTAC 3396
QY 1078 AlaProProGlyHisProLeuProLysGluLysAspThrAlaAspProValLeuPro 1097

QY 1814 IleLeuThrSerThrThrThrValGluHisAlaProIleThrArgProGlyThrIleGlu 1833
DB 5473 ATCTTCACCTGTACACATACAGTGGAGCATGACCATCTGGAGACCTGGTACGGAGCAG 5532
QY 1834 SerSerGlySerSerGlySerGlyGlyGlyGlyGlyGlySerSerArgProAlaSer 1853
DB 5533 AGCAGCGGGGCT-----GGGGGACGAGCGCGCGCGCTCC 5568
QY 1854 HisSerHisAlaHisGlnHisSerProIleSerProArgThrGlnHisAlaLeuGln 1873
DB 5569 CACACC-----CACAGCACTGGCCCATCTCCCGGACCGAGACGCTTGAGCAG 5622
QY 1874 ArgProSerValLeuHisAsnThrGlyMetLysGlyIleIleThrAlaValGluProSer 1893
DB 5623 AGGCCCAAGTGTCTGCACACACAGAGCATGAAGGGCGTGTACCTCCGTGGAAACCCGCG 5682
QY 1894 LysProThrValLeuArgSerThrThrSerSerProValArgProAlaAlaThrPhe 1913
DB 5683 ACGCCCAACGGTCTGAGGTCCACCTCCACCTCTTCGCTGTCCGCCAGCTGCCACATTC 5742
QY 1914 ProProAlaThrHisCysProLeuGlyGlyThrLeuAspGlyValTyProThrLeuMet 1933
DB 5743 CCACCTGCCACCACTGCCCACTTTGGTGGCACCTTTGAAGGGGTCTACCTTACCTCATG 5802
QY 1934 GluProValLeuProLysGluAlaProArgValAlaArgProGluArgProArgAla 1953
DB 5803 GAGCCCGTCTCTGTACCCAGAGAGCTCTCGGGTGGCGCCCGGCCGAGCGGCCCGGTGTG 5862
QY 1954 AspThrGlyHisAlaPheLeuAlaLysProProAlaArgSerGlyLeuGluProAlaSer 1973
DB 5863 GAGGTGGCGATGCTCTCTCCACCAACCCCGGCCGCG-----GAGCCCGCTCC 5913
QY 1974 SerProSerLysGlySerGluProArgProLeuValProProValSerGlyHisAlaThr 1993
DB 5914 TCACCCAGCAAGAGCTCCGAGCCCGCATCTCCCTAGCACCCCGGAGCTCCAGCCACACAGCC 5973
QY 1994 IleAlaArgThrProAlaLysAsnLeuAlaProHisHisAlaSerProAspProAla 2013
DB 5974 ATGCCCGCACCCAGCAAGAGCTTGACCCACCCACCATGCTCGAGTCGGAGCCGCGCGGG 6033
QY 2014 ProProAlaSerAlaSerAspProHisArgGluLysThrGlnSerLysProPheSerile 2033
DB 6034 ---CCACCTCGGCTCAGATCTGCACCGAGAAAGATCAAGTAAACCTTTTCCATC 6090
QY 2034 GlnGluLeuGluLeuArgSerLeuGlyTyHis---GlySerSerTySerProGluGly 2052
DB 6091 CAGGAATTCGAATCCGTTCTCTGGGTACCAAGTGGAGCTGGCTACAGCCCGCATGGG 6150
QY 2053 ValGluProValSerProValSerSerProHisArgGluLysThrGlnSerLysProPheSerile 2072
DB 6151 GTGAGGCCCATCAGCCCGGTGAGCTTCCCGAGCTTCCCGAGCTTCCCGAGCGGCTTCCAAA 6210
QY 2073 HisLeuGluGluLeuAspLysSerHisLeuGluGlyGluLeuArgProLysGlnProGly 2092
DB 6211 CCTCTGGAAGAGCTAGAGAGAGCCACTTGGAAAGGGAGCTGGCGCACAGAGCCAGCGC 6270
QY 2093 ProValLysLeuGlyGlyGluAlaAlaHisLeuProHisLeuArgProLeuProGluSer 2112
DB 6271 CCCATGAGCTCAGCGCGGAGGCTGCCCATCTCCACATCTCGGGCCACTGCCCGAGAGC 6330
QY 2113 GlnProSerSerSerProLeuLeuGlnThrAlaProGlyValLysGlyHisGlnArgVal 2132
DB 6331 CAGCCCTCATCCAGCCCATCTCTCCAGCTTCCCGAGCTTCCCGAGCTTCCCGAGCGG 6390
QY 2133 ValThrLeuAlaGlnHisIleSerGluValIleThrGlnAspTyThrArgHisPro 2152
DB 6391 GTCACCTTGGCTCAGCATCATCAGCAGAGGTCAATACGAGGACTACACCCGCGCACCCCG 6450
QY 2153 GlnGlnLeuSerAlaProLeuProAlaProLeuTySerPheProGlyAlaSerCysPro 2172
DB 6451 CAGCAGCTCAGTGGGCCCTTCCCGCCCTCTCTACTCTCTTTCGGGAGCCAGCTGCCCT 6510
QY 2173 ValLeuAspLeuArgArgProProSerAspLeuTyLeuProProProAspHisGlyAla 2192

DB 6511 GTGTGTGATCTTCGGCGGCCACCCAGTGACCTTACTCTCCACCCCGCCACCATGGCACC 6570
QY 2193 ProAlaArgGlySerProHisSerGluGlyGlyLysArgSerProGluProAsnLysThr 2212
DB 6571 CCAGCCCGGGGTTCCTCCCCACAGTGAAGGGGCAAAAGGTCTCCACAGAACCCAGCAAAACA 6630
QY 2213 SerValLeuGlyGlyGlyGluAspGlyIleLeuProValSerProProGluGlyMetThr 2232
DB 6631 TCGGTCTCTGGGAGAGCAGTGTGAGATGCCATGTGACCTGTGTCCACACAGAGGATGACT 6690
QY 2233 GluProGlyHisSerArgSerAlaValTyProLeuLeuTyArgAspGlyGluGlnThr 2252
DB 6691 GAGCCAGGACATGCTCGGAGGGCTGTGTACCCACTGTCTATCCAGAGCGGGAAACAGGC 6750
QY 2253 GluProSerArgMetGlySerLysSerProGlyAsnThrSerGlnProProAlaPhePhe 2272
DB 6751 GAGCCC---AGATGGGCTCTAAGTCTCCAGGCAACACCCAGCCAGCGCCCTTCTTC 6807
QY 2273 SerLysLeuThrGluSerAsnSerAlaMetValLysSerLysGlnGlnIleAsnLys 2292
DB 6808 AGTAAGCTGACGAGAGCACTCCGCCATGTGTAAGTCGAAGAGCGAGGATCAACAG 6867
QY 2293 LysLeuAsnThrHisAsnArgAsnGluProGluTyAsnIleSerGlnProGlyThrGlu 2312
DB 6868 AAATCTCAACACACACAAACCGGAAACGAGCCAGATAAATATTGGCCAGCTTGGGACGAA 6927
QY 2313 IlePheAsnMetProAlaIleThrGlyThrGlyLeuMetThrTyArgSerGlnAlaVal 2332
DB 6928 ATCTTCAACATCCCGCCCATCATCTGGAGCAGGCTTATGACCTGTAGAACCCAGCGGTG 6987
QY 2333 GlnGluHisAlaSerThrAsnMetGlyLeuGluAlaIleIleArgLysAlaLeuMetGly 2352
DB 6988 CAAGAACACCGCAGACCAACCATGGGCTAGAGGCCATTTATTAGAAAGGCACATCAGGGT 7047
QY 2353 LysTyAspGlyTrpGluGluSerProProLeuSerAlaAsnAlaPheAsnProLeuAsn 2372
DB 7048 AAATATGATCATTTGGAAAGAGCCCGCCGCTCGGCGCAATGTCTTTTAACTCTGAAT 7107
QY 2373 AlaSerAlaSerLeuPro---AlaAlaMetProIleThrAlaAlaAspGlyArgSerAsp 2391
DB 7108 GCCAGCCCGCTGCTCCGCTGTCTGTATGCCATTAACCATGTCTGACGACGAGTGAC 7167
QY 2392 HisThrLeuThrSerProGlyGlyGlyLysAlaLysValSerGlyArgProSerSer 2411
DB 7168 CACGCACTCATCTCCCGAGGGTGGAGTGGGAAGCCAAAGTCTCTGGCAGACCTAGCAGC 7227
QY 2412 ArgLysAlaLysSerProAlaProGlyLeuAlaSerGlyAspArgProProSerValSer 2431
DB 7228 CGAAGGCCAATTCGCCAGCACACGCTAGCGTCCGGAGCCGACCCCTTCTGTCTCC 7287
QY 2432 SerValHisSerGlyAspCysAsnArgArgThrProLeuThrAsnArgValTrpGlu 2451
DB 7288 TCAGTACATCTCAGGGGATGCAATCGCCGAACACCACTCACCACCGGTGTGGAG 7347
QY 2452 AspArgProSerSerAlaGlySerThrProPheProTyAsnProLeuIleMetArgLeu 2471
DB 7348 GACCGGCCCTCTCTGCAAGGGTCCACGCCATTCCTCCCTCAACCTTTGATTATGAGGCTA 7407
QY 2472 GlnAlaGlyValMetAlaSerProProProGlyLeuProAlaGlySerGlyProLeu 2491
DB 7408 CAGCGAGGTGTATGGCTTCCCGCCCTCCCGCTTGGCGCAGCAGCGGGCCCTTA 7467
QY 2492 AlaGlyProHisHisAlaTrpAspGluProLysProLeuLeuCysSerGlnTyGlu 2511
DB 7468 GCTGGTCCCCCAGCGCTGGATGAGAGGCCCAAGGACCTGTGTGTTCACAGTATGAG 7527
QY 2512 ThrLeuSerAsnSerGlu 2517
DB 7528 ACATCTCCGAGAGCGAG 7545

Db	2660	GGACACAGTACCCCCAAAGCCAGTTTCCCTCTGCTGCTCCACCCAGCAGCACTACAGCC	2711
Qy	1007	odluserAspAlaProGlnInProGlySerProArgGlyLysSerArgSerProAl	1027
Db	2720	AGAGGGTGAAGTGTCTCAGCAGTGGGAGGAGTCCAGTGGCAAGTCCGAGCAGCCAGT	2779
Qy	1027	aProAlaAspLysGlu-----AlaPheAlaAspAla	1039
Db	2780	GCCTCTCGCGAGAGAGGACAGAAACCGCATCTTTCGGCTTCCCACTGAGGG	2839
Qy	1039	aGlnLysLeuProGlyYAspProProCyThrThrSerGlyLeuProPheProValProPr	1059
Db	2840	CCCAAGAGTACCAGTGAAGCCCCACAGCTGGTCATCGGGCTGCTTCCCATCCTCC	2899
Qy	1059	oArgGluValLysAlaSerProHisAlaProAspProSerAlaPheSerTyrAlaPr	1079
Db	2900	ACGGAGGTGATCAGACTTCCACACAGCGCTGACCCCTCTGCTCTCTCTACACACC	2959
Qy	1079	oProGlyHisProLeuProLeuGlyLeuHisAspThrAlaArgProValLeuProArgPr	1099
Db	2960	CCCCGGTCAACCGCTGCTTGGGCTTCCAGTAGTGCCCGGCGCTGCTGCGACGTCC	3019
Qy	1099	oProThrLysSerAsnProProLeuLysSerSerAlaLysHisProSerValLeuGln	1119
Db	3020	CCCC---ATCTTAACCCCCCACCCTCATCTCTGCTGCAAGCATCCCGGGGTACTTGA	3076
Qy	1119	uArgGlnLysAlaLysSer---GlnGlyMetSerValGlnLeuHisValProTyrSe	1138
Db	3077	GAGGCAGCTGGGTGCCATCTCCACAGCAGGGGATGTCACTCCAGCTGCTGCTCACTC	3136
Qy	1138	rGluHisAlaLysAlaProValGlyProValThrMetGlyLeuProLeuProMetAspPr	1158
Db	3137	AGAGCATGCCAAGCCCCCTGCGGCTCTCACCATGGGGCTGCCCCCTGCGTGAGACC	3196
Qy	1158	oLysLysLeuAlaProPheSerGlyValLysGlnGlnLeuSerProArgGlyGlnAl	1178
Db	3197	TAAAGACTG-----	3206
Qy	1178	adLysProGlySerLeuGlyValProThrAlaGlnGluAlaSerValLeuArgGlyTh	1198
Db	3207	-----GGGAC	3211
Qy	1198	rAlaLeuGlySerValProGlyGlySerLysThrLysGlyLeuProSerThrArgValPr	1218
Db	3212	AGCACTGGGTCCGCCACCATGGAGCATCACCAAGGGCTTCCCCAGTACCCGGGTGTC	3271
Qy	1218	oSerAspSerAlaLysThrTyrArgGlySerLysThrHisGlyThrProAlaAspValLe	1238
Db	3272	AGACGGCCCC---AGTACAGAGGCTCTATCATCCACCGCACGCCCGCAGACGTCTCT	3325
Qy	1238	uTyrLysGlyThrLysThrArgLysLeuGlyLeuAspSerProSerArgLeuAspArgL	1258
Db	3326	CTACAGGGTACCATCAGCAGGATCGTGGTGAGCAGACCCCAAGTCTGCTTACCGGGC	3385
Qy	1258	YArgGluAspSerLeuProLysGlyHisValLysThrGluLysLysGlyHisValLe	1278
Db	3386	ACGAGAGACACCTTCCCAAGGCGCATGTCATCTATGAGGGCAGAAAGGCCAGCTCT	3445
Qy	1278	uSerTyrGluGlyGlyMetSerValThrGlnCysSerLysGluAspGlyArgSerSerSe	1298
Db	3446	ATCTATGAAGTGGTATGTCCTGCTCAGAGTGCTCTAAGGAGGATGGAAGGAGCAGCTC	3505
Qy	1298	rGlyProProHisGluThrAlaAlaProLysArgThrTyrAspMetMetGluGlyArgGva	1318
Db	3506	GGGCCCCCATGAGACTGCGGCCCTTAACGCACCTATGACATGATGAGGGCCGTGT	3565
Qy	1318	lGlyArgAlaLysSerSerAlaSerLysGluGlyLeuMetGlyArgAlaLysProProGl	1338
Db	3566	AGGCAGGACTGTCTCAGTCAGCAGATGAGGGGATCTCATGGGCGCGGCCATC---CCTGA	3622
Qy	1338	uArgHisSerProHisHisLeuLysGluGlnHisLysLysLysLysLysLysLysLysLys	1358
Db	3623	GCAGCAGCCCC---CACTTCAAGGAGGAGATCATCTCCAGGCTTCCACAGCAGCAAGG	3679

Qy	1358	YlleProArgSerTyrValGluAlaGlnGluAspTyrLeuArgArgGluAlaLysLeuLe	1376
Db	3680	CATCCCGAGGTTCTATGTGAGCGCAGAGAGACTACTTACGGCGGAGGCCAGCTCTT	3739
Qy	1378	uLysArgGluGlyThrProProProProProSerArgAspLeuThrGluAlaTyrLy	1398
Db	3740	GAAGCGAGAAGGAGACACACACCCACACCACTTCGGGACCTGACTGAGACTACAA	3799
Qy	1398	sThrGln-----AlaLeuGlyProLeuLysLeuLysProAlaHisGluGlyLeuVa	1415
Db	3800	GCCCGCGGCCCTGGACCTCTCGGGTCCCTGAAGCTGAAGCCGACTCACGAGGGTGGT	3859
Qy	1415	lAlaThrValLeuGluAlaGlyArgSerLysHisGluLysLeuProArgGluGluLeuArgHi	1435
Db	3860	AGCACTGTGAGAGAGCGGGCGCGCTTATCATGAGATCCCGAGAGAGAGCTGCGCCG	3919
Qy	1435	sThrProGluLeuProLeuAlaProArgProLeuLysGluGlySerLysLeuThrGlnGlyTh	1455
Db	3920	CACACTGAGCTAACCCCTGCGACCAAGCGCTCTGAAGAGGGTTCCATCACCCAGGCGAC	3979
Qy	1455	rProLeuLysTyrAspThrGlyAlaSerThrThrGlySerLysLysHisAspValArgSe	1475
Db	3980	CCCACTCAAGTACGACTCTGGGGACCCCTCCACTGGCACCAAGAAACACGACGTGGCGCTC	4039
Qy	1475	rLeuLiedGlySerProGlyArgThrPheProProValHisProLeuAspValMetAlaAs	1495
Db	4040	CATCATCGGCAGCCCGCGCGCGCTTCCCTGCCCTGCACCCGCTGGACATAATGGCTGA	4099
Qy	1495	pAlaArgAlaLeuGluArgAlaCysTyrGluLysSerLeuLysSerArgProGlyThrAl	1515
Db	4100	CGCCCGGGGACAGAGAGGTGCGCTGTATGAGAGAGTCTGAGAGCCGCTCAGGAGCCAG	4159
Qy	1515	aSerSerSerGlyGlySerLysLeuAlaArgGlyAlaProValLysLeuProGluLeuGlyLy	1535
Db	4160	CAGTGTGTGCAGCGGGCTCCATCACAGCTGGGGGCTCCAGTGGTGGCTGAACTGGGCAA	4219
Qy	1535	sProArgGlnSerProLeuThrTyrGluAspHisGlyAlaProPheAlaGlyHisLeuPr	1555
Db	4220	GCCACGGCAAAAGCCCACTGACTTAGAAGACACAGGGGACCGCTTCCACAGTCACTGCC	4279
Qy	1555	oArgGlySerProValThrMetArgGluProThrProArgLeuGlnGluGlySerLeuSe	1575
Db	4280	ACGTGGCTCCCGTGTGACACACGNGGGAGCCACGCCGCTTACAGAGGCGAGCTCTCT	4339
Qy	1575	rSerSerLysAlaSerGluAspArgGlyLeuThrSerThrProArgGluLeuAlaLysSe	1595
Db	4340	ATCCAGCAAGGTGTCCAGACCGGAGCTGACATCTACACCCGGGAGATCGCAAGTC	4399
Qy	1595	rProHisSerThrValProGluLysHisProHisProLysSerProTyrGluHisLeuLe	1615
Db	4400	CCACACAGACATGTGCCCGGACACACCTTCAACCCCATCTCCCTCCCTATGAGCACTTGC	4459
Qy	1615	uArgGlyValSerGlyValAspLeuTyrArgSerHisLysProLeuAlaPheAspProTh	1635
Db	4460	CGGGGCGTGAAGTGTGTGACCTGTACCGTGGTGCATCCCATTTGGCTTTTGAACCCAC	4519
Qy	1635	rSerLysProArgGlyLeuProLeuAsp--AlaAlaAlaTyrTyrLeuProArgHi	1654
Db	4520	CTCCATACCCCGGGATCCCTCTGGAAGCAGCAGCGGCGCTACTACTCTGCCCGGCA	4579
Qy	1654	sLeuAlaProArgProThrTyrProHisLeuTyrProProTyrLeuLysGlyTyrPr	1674
Db	4580	CTTGGCCCCCAACCCCACTTCCACACTGTACCCACCTTACCTTATCTCCGCGCTATCCC	4639
Qy	1674	oAspThrAlaAlaLeuGluAsnArgGlnThrLysLysAsnAspTyrLysThrSerGlnG	1694
Db	4640	TGACACGCGCGCTCGAGAACCGCCAGACCATCATCATGACTACATCATCACTCGCAGCA	4699
Qy	1694	nMetHisHisAspThrAlaThrAlaMetAlaGlnArgAlaAspMetLeuArgGlyLeuSe	1714
Db	4700	GATGACCAACATGCTGCTCCCTCCGATCGGCCAGCTGCTGACATGCTGAGGGGCTGTGC	4759

QY 1714 rProArgGluSerSerLeuAlaLeuAenTyrAlaAlaGlyProArgGlyLeileAspLe 1734
DB 4760 ACCGCGAGAGTCTCGCTGGCCCTCAATTATCGCTGGCCGAGAGGCAATATCGACCT 4819
QY 1734 uSerGlnValProHisLeuProValLeuValProProThrProGlyThrProAlaThrAl 1754
DB 4820 GTCCCAAGTGGCCACACCTGCGCGGTGTGTGTGCACACACGCGAGGACCCCTGCCACCGC 4879
QY 1754 aMetAspArgLeuAlaTyrLeuProThrAlaProGlnProPheSerSerArgHisSerSe 1774
DB 4880 CATCGACCGCTTGGCTACCTCCGCTCCGCTGGCCGACCCCTTCAGCAGCGCCACAGTAG 4939
QY 1774 rSerProLeuSerProGlyGlyProThrHisLeuThrLysProThrThrThrSerSerSe 1794
DB 4940 CTACCGCTGTCCCGAGGCGCCCACTCACCTAGCTAAACCACTGCCACATCTTCATC 4999
QY 1794 rGluArgGluArgAspArgAspArgGluArgAspArgGluArgGluLysSerIl 1814
DB 5000 GGAGCGGGAACGGGACCTGAGCGGGAACGAGAC-----AAGTCCAT 5041
QY 1814 eLeuThrSerThrThrValGluHisAlaProIleTrpArgProGlyThrGluGlnSe 1834
DB 5042 CCTCAGCTCTACCACTACAGTGGAGCATGACCCCATCTGGAGACCTGGTACGGAGCAGAG 5101
QY 1834 rSerGlySerSerGlySerGlyGlyGlyGlyGlyGlySerSerArgProAlaSerHi 1854
DB 5102 CAGCGGGGCT-----GGGGGCGAGCGCGCGCCCTCCCA 5137
QY 1854 sSerHisAlaHisGlnHisSerProIleSerProArgThrGlnAspAlaLeuGlnLar 1874
DB 5138 CACC-----CACCAGCAGCTCGCCCATCTCCCGCCGACCCAGAGCGCTTCGACGAG 5191
QY 1874 gProSerValLeuHisAenThrGlyMetLysGlyIleIleThrAlaValGluProSerLy 1894
DB 5192 GCCCAGTGTGTGCACACACGAGCATGAAGGCGTGTGTACCTCGGTGGAACCGCGCAC 5251
QY 1894 sProThrValLeu-----ArgSerThrSerThrSerProValArgProAlaAl 1911
DB 5252 GCCCAGGCTCTGAGTGGGCGAGTCCACTTCCACTTTCGCTGTTCGCGCCAGCTGC 5311
QY 1911 aThrPheProAlaThrHisCysProLeuGlyGlyThrLeuAspGlyValTyrProTh 1931
DB 5312 CACATTCCTCACCTGACACCTGCGCCACTTGGTGGCCCTTGAAGGGGTCTACCTTAC 5371
QY 1931 rLeuMetGluProValLeuLeuProLysGluAlaProArgValAlaArgProGluArgPr 1951
DB 5372 CCTCATGGAGCGCGTCTGTGTACCAAGGAGACCTCTCGGTGCGCGCGCGCGCGCGGC 5431
QY 1951 oArgAlaAspThrGlyHisAlaPheLeuAlaLysProProAlaArgSerGlyLeuGluPr 1971
DB 5432 CCGGTGGAGCGTGGCCATGCTTTCTTACCAACCCCGGGCGG-----GAGCC 5482
QY 1971 oAlaSerSerProSerLysGlySerGluProArgProLeuValProProValSerGlyHi 1991
DB 5483 CGCCTCTCACCCAGCAGAGCTCGAGCCCGGATCTTACACCCCGCCAGCTCCAGCCA 5542
QY 1991 sAlaThrIleAlaArgThrProAlaLysAenLeuAlaProHisHisAlaSerProAspPr 2011
DB 5543 CACAGCATCGCCCGCCAGCCAGCAAGAACCTTCACCCCACTCCAGCTCCGAGCC 5602
QY 2011 oProAlaProAlaSerAlaSerAspProHisArgGluLysThrGlnSerLysProPh 2031
DB 5603 CCGCGG-----CCACCTCGGCTCAGATTCGACCGAGAAAGACTCAAGTAAACCTT 5659
QY 2031 eSerIleGlnLeuGluLeuArgSerLeuGlyTyrHis---GlySerSerTyrSerPr 2050
DB 5660 TTCATCTCAGGAATGGAACTCCGTTCTCTGGGTATACCAAGTGGAGCTGGGTACAGCC 5719
QY 2050 oGluGlyValGluProValSerProValSerProSerLeuThrHisAlaLysGlyLe 2070
DB 5720 CGATGGGTGGAGCCCATCAGCCCGGTGAGCTCCCGAGCTTCGACCAACGACGAGGGGCT 5779
QY 2070 uProLysHisLeuGluGluLeuAspLysSerHisLeuGluGlyLeuArgProLysG 2090

DB 5780 CTCCAAACCTCTGGAAGAGCTAGAGAGGAGCCATTGGAAGGGAGCTGGCGCACAGCA 5839
QY 2090 nProGlyProValLysLeuGlyGlyGluAlaAlaHisLeuProHisLeuArgProLeuPr 2110
DB 5840 GCCAGGCCCATTAAGCTCAGCGGAGGCTGCCCATCTCCACATCTCGGGCCACTGCC 5899
QY 2110 oGluSerGlnProSerSerSerProLeuLeuGlnThrAlaProGlyValLysGlyHisG 2130
DB 5900 CGAGAGCAGCGCTCATCCGCCACTCTCCAGACTGCCCGAGCATCAAGAGTCAACA 5959
QY 2130 nArgValValThrLeuAlaGlnHisIleSerGluValIleThrGlnAspTyrThrArgHi 2150
DB 5960 GAGGTTGGTCACTCTGGCTCAGCATCAGCAGAGTCAATACGAGGACTACACGGCCA 6019
QY 2150 sHisProGlnGluSerAlaProLeuProAlaProLeuTyrSerPheProGlyAlaSe 2170
DB 6020 CCACCGCGAGCTCTCAGTGGCCCTTCCCGCCCTCTCTACTCTCTTCCGGAGCCAG 6079
QY 2170 rCysProValLysLeuLeuArgArgProProSerAspLeuTyrLeuProProPheP 2190
DB 6080 CTGCCCTGTCTGGATCTTCGCCGCCACCCAGTGAACCTCTACCTCCACCCCGCCACCA 6139
QY 2190 sGlyAlaProAlaArgGlySerProHisSerGluGlyGlyLysArgSerProGluProAs 2210
DB 6140 TGGCACCCAGCTCGGGCATCCGCCACACACTGAAGGGGCAAAAGTCTCCAGAACCCAG 6199
QY 2210 nLysThrSerValLeuGlyGlyGluAspGlyIleGluProValSerProProGluG 2230
DB 6200 CAAACATCGCTCTGGGCACGAGGATGCCATTAGCTGTGTCCCAACAGAGG 6259
QY 2230 yMetThrGluProGlyHisSerArgSerAlaValTyrProLeuLeuTyrArgAspGlyG 2250
DB 6260 CATGACTGAGCAGGACATGTCTGGAGACTGTGCTACCCACTGTGTATCGAGCGGGA 6319
QY 2250 uGlnThrGluProSerArgMetGlySerLysSerProGlyAenThrSerGlnProProAl 2270
DB 6320 ACAGGCGAGCG-----AGGATGGTCTAGAGTCTCCAGCAACACAGCGCGCCAA 6376
QY 2270 aPhePheSerLysLeuThrGluSerAenSerAlaMetValLysSerLysGlnGluI 2290
DB 6377 CTCTTCAGTATCTGACTGAGACAACTCCGCCATGTGTGAAGTCGAGAGCGAGAT 6436
QY 2290 aEnLysLeuLeuAenThrHisAenArgAenGluProGluTyrAenIleSerGlnProG 2310
DB 6437 CAACAAGAAACTAAACACCCCAACCGGAACGAGCGCAATACATAATATTGGCCAGCTGG 6496
QY 2310 yThrGluIlePheAenMetProAlaIleThrGlyThrGlyLeuMetThrTyrArgSerG 2330
DB 6497 GACGGAATCTTACATGCTCCCGCCATCACTGGAGCGGCTTATGACCTGTAGAAGCCA 6556
QY 2330 nAlaValGlnGluHisAlaSerThrAenMetGlyLeuGluAlaIleArgLysAlaLe 2350
DB 6557 GCGGTGCAAGAACAGCCGACCAACATGGGGCTAGAGCCCATTTATGAAGGACT 6616
QY 2350 uMetGlyLysTyrAspGlnTrpGluGluSerProProLeuSerAlaAenAlaPheAenPr 2370
DB 6617 CATGGTAAATTTGATCAGTGGGAAGAGCCCGCGCTCGCGCCCAATGCTTTAACCC 6676
QY 2370 oLeuAenAlaSerAlaSerLeuPro---AlaAlaMetProIleThrAlaAlaAspGlyAr 2389
DB 6677 TCTGAATGCCAGCGCCAGTCTGCCGCTGTGCTATGCCCATACCACTCTCTGACCGAG 6736
QY 2389 gSerAspHisThrLeuThrSerProGlyGlyGlyLysAlaLysValSerGlyArgPr 2409
DB 6737 GAGTGACCACTGACTCCTCCCTCGCAGTGGAGTGGGAARGCCAAAGTCTCTGGCAGACC 6796
QY 2409 oSerSerArgLysAlaLysSerProAlaProGlyLeuAlaSerGlyAspArgProProSe 2429
DB 6797 TAGCAGCCGAATAGGCAAGTCCGAGCACCGAGCCCTAGCGTCCGAGAGACGAGCCCTTC 6856
QY 2429 rValSerSerValHisSerGluGlyAspCysAenArgArgThrProLeuThrAenArgVa 2449

Db	819	GGTCAGCTCCACGTCCTCCAGAGCATGCAAGGCCCGGTGGGCGCTGTCCACAT	878	QY	1510	rArgProGlyThrAlaSerSerGlyGlySerIleAlaAArgGlyValaProValIleVa	1530
QY	1150	tGlyLeuProLeuProMetAspProLysLysLeuAlaProPheSerGlyValIysGlnG	1170	Db	1959	CGGGCCAGGAGGAGCCAGCAGAGTCTGGGGGGGTCTCCATGTGCGCGCGCGCCGGTCATTGT	2018
Db	879	GGGGCTGCGCTCCCTCCATGACCCCAAAAGCTGGCACCCCTTCAGCGGAGTGAAGCAGA	938	QY	1530	lProGlyLeuGlyValProArgGlnSerProLeuThrTyrGluAaspHisGlyAlaProPh	1550
QY	1170	uGlnLeuSerProArgGlyGlnAlaGlyProProGlnSerLeuGlyValProThrAlaG	1190	Db	2019	GCTGAGCTGGGAAGCGCGGCGAGAGCCCTGACCTATGAGGACCAACGGGACCCCTT	2078
Db	939	GCAGCTGTCCCAAGGGCCAGGCTGGGCCACCGAGAGCCCTGGGGGTGGCCACGCCA	998	QY	1550	eAlaGlyHisLeuProArgGlySerProValThrMetArgGluProThrProArgLeuG	1570
QY	1190	nGluAserValLeuArgGlyThrAlaLeuGlySerValProGlyGlySerIleThrI	1210	Db	2079	TCCCGGCCACCTTCCACAGAGTTCCCGGTGACCATCGGGAGCCACGCGCGCCGTGCA	2138
Db	999	GGAGGCGCTCGCTGAGAGGACAGCTCTGGGCTCAGTTCCGGCGGAAAGCATCACAA	1058	QY	1570	nGlyGlySerIleAlaSerSerLysAlaSerGlnAaspArgLysLeuThrSerThrProAr	1590
QY	1210	sGlyIleProSerThrArgValProSerAspSerAlaIleThrTyrArgGlySerIleTh	1230	Db	2139	GGAGGGCAGCCCTTGTCCAGCAAGGCATCCAGAGCCGAAAGCTGAGTGAGCGCCTCG	2198
Db	1059	AGGCATTTCCACAGCACACGGGTGCTCGGACAGCGCCATCACATACCGCGGCTCCCATC	1118	QY	1590	gGluIleAlaLeuSerProHisSerThrValProGluHisHisProHisProIleSerPr	1610
QY	1230	rHisGlyThrProAlaAspValLeuTyrLysGlyThrIleThrArgIleIleGlyGluAs	1250	Db	2199	TGAGATCGCCAGTCCCGGACAGACCCGTGCTCCCGAGCACCCACCCACCCCATCTGCC	2258
Db	1119	CCAGCGCACGCCAGCTGACGCTCTGTACAGGGGACATCACAGAGATCATTCGGCGAGA	1178	QY	1610	oTyrGluHisLeuLeuArgGlyValSerGlyValAaspLeuTyrArgSerHisIleProLe	1630
QY	1250	pSerProSerArgLeuAaspArgGlyAArgLysAaspSerLeuProLysGlyHisValIleTy	1270	Db	2259	CTATGAGCACCTTCTTGGGGGGGTGAGTGGCGTGGACCTGTATCGCGAGCCACATCCCCCT	2318
Db	1179	CAGCCCGAGTGGCTTGGACCGCGCGGAGGACAGCTTGGCCCAAGGGCCACGTCATCTA	1238	QY	1630	uAlaPheAaspThrSerIleProArgGlyIleProLeuAaspAlaAlaAlaIleTyrTy	1650
QY	1270	rGluGlyLysLysGlyHisValLeuSerTyrGluGlyGlyMetSerValThrGlnCysSe	1290	Db	2319	GGCCTTTCAGCCCTACCTCCATACCCCGCGGCATCCCTCTGGACGCGAGCGCTGCTACTA	2378
Db	1239	CGAAGGCAAGAGGGCCAGCTCTTGTCTATGAGGGTGGCATGTCTGTGACCCAGTGCTC	1298	QY	1650	rLeuProArgHisLeuAlaProAspProThrTyrProHisLeuTyrProProTyrLeuI	1670
QY	1290	rLysGluAaspGlyArgSerSerGlyProProHisGluThrAlaAlaProLysArgTh	1310	Db	2379	CTGCCCCGAGACTGGCCCCCACCACCCCTACCCGACCTGACCTACCCACCTACCTCAT	2438
Db	1299	CAGGGAGGAGCGGAGAGCAGCTCAGACCCCCCCCCATGAGACGGCGCCCCCAAGGGCAC	1358	QY	1670	eArgGlyTyrPheAaspThrAlaAlaLeuGluAaspArgGlnThrIleIleAaspTyrI	1690
QY	1310	rTyrAaspMetGluGlyArgValGlyArgAlaIleSerSerAlaSerIleGluGlyLe	1330	Db	2439	CGCGGGTATCCGACACACGCGCGCGCTGGAGAACCGGACGACCATCATCATGACTACAT	2498
Db	1359	CTATGACATGATGAGGGCGCGGTGGGCGAGAGCATCTCTCTCAGCCAGCATCGAAGGTCT	1418	QY	1690	eThrSerGlnGlnMetHisHisAsnThrAlaThrAlaMetAlaGlnArgAlaAaspMetLe	1710
QY	1330	uMetGlyArgAlaIleProProGluAArgHisSerProHisHisLeuLysGluGlnHisH	1350	Db	2499	CACCTCGCAGCGATGCACACCAACAACACCGCCACCGCCATGGCCGAGCGGTGATGCT	2558
Db	1419	CATGGCGGTGCCATCCCGCGAGCGACACAGCCCCCAACCTCAAGAGAGGACACCA	1478	QY	1710	uArgGlyLeuSerProArgLysSerIleAlaLeuAaspTyrAlaAlaGlyProArgG	1730
QY	1350	sIleArgGlySerIleThrGlnGlyIleProArgSerTyrValGluAlaGlnGluAepTy	1370	Db	2559	GAGGGGCTCTGCGCCCCGGAGTCTCTCGCTGGCACTCACTACGCTGGGGGTCCCGGAGG	2618
Db	1479	CATCGGGGTCCATCACAAAGGATCCCTCGGTCTCTACGTGGAGGCGACAGGAGACTA	1538	QY	1730	yIleIleAaspLeuSerGlnValProHisLeuProValLeuValProThrProGlyTh	1750
QY	1370	rLeuArgArgGluAlaLysLeuLysAArgGlyThrProProProProProSe	1390	Db	2619	CATCATCGACCTTCCCAAGTGCACACCTGCTGTGCTGTCGCCCGCCGACACAGGAC	2678
Db	1539	CCTGCGTGGGAGGCCAAGCTCTTAAAGGGGAGGCGACGCGCTCCGCCCCCACCGCCCTC	1598	QY	1750	rProAlaThrAlaMetAaspArgLeuAlaTyrLeuProThrAlaProGlnProPheSerSe	1770
QY	1390	rArgAspLeuThrGluAlaTyrLysThrGlnAlaLeuGlyProLeuLysIleuLysProAl	1410	Db	2679	CCAGCCACCGATGACGCGCTTGCCTACTCCACCGCGCCCGCCAGCCCTTCAGCAG	2738
Db	1599	ACGGAGCTCAGCGAGGCTTACAGACGAGGCGCTGGGCGCCCTCGAAGCTGAGGCGCG	1658	QY	1770	rArgHisSerSerProLeuSerProGlyGlyProThrHisLeuThrLysProThrTh	1790
QY	1410	aHisGluGlyLeuValAlaThrValLysGluAlaGlyArgSerIleHisGluIleProAr	1430	Db	2739	CGCCACAGCAGCTTCCCTCCCTCCAGAGGTCCCAACACACTTGACAAACCAACACAC	2798
Db	1659	CCATGAGGGCTGCTGGCCACCGGTGAAGAGGCGGCGCTCTCATTCATGAGATCCCGCG	1718	QY	1790	rThrSerSerSerGluArgGluArgAaspArgGluArgAaspArgAaspArgGluAr	1810
QY	1430	gGluGluLeuArgHisThrProGluLeuProLeuAlaProArgProLeuLysGluGlySe	1450	Db	2799	CACGTCTCTGTGAGCGGAGGACAGACCGGGATCGAGAGCGGAGCCGCGGATCGGAGCG	2858
Db	1719	CGAGAGCTGGGACACACGCCCGAGCTGCCCTTGGCCCGCGCGCGCTCAAGAGGGGCTC	1778	QY	1810	gGlyLysSerIleLeuThrSerThrThrValGluHisAlaProIleTyrArgProG	1830
QY	1450	rIleThrGlnGlyThrProLeuLysTyrAspThrGlyAlaSerThrThrGlySerLysI	1470	Db	2859	GGAAAGTCCATCTCATCTCCACCGAGCGGTGGAGCAGCCACCCATCTGGAGACTGG	2918
Db	1779	CATCAGCGGGCACCCCGCTCAAGTACGACACCGGGGCTCCACCACTGGCTCCAAAAA	1838	QY	1830	yThrGluGlnSerSerGlySerSerGlySerSerGlyGlyGlyGlyGlySerSerAr	1850
QY	1470	sHisAaspValArgSerLeuIleGlySerProGlyArgThrPheProValHisProLe	1490	Db	2919	TACAGAGCAGCAGAGCGGAGCGGCGAGCGCGGGGGTGGGGGCGAGCAGCAGCCG	2978
Db	1839	GCAGGAGTACGCTCCCTCATCGGCGAGCCCGCGCGGAGGTTCACACCGCTGACCCGCT	1898	QY	1850	gProAlaSerHisSerHisAlaHisGlnHisSerProIleSerProArgThrGlnAaspAl	1870
QY	1490	uAaspValMetAaspAlaAaspAlaLeuGluAArgAlaCysTyrGluGlnSerLeuLysSe	1510	Db	2979	CCCCGCTCCCATCTCCCATGCCACACGACCTGCCCCATCTCCCTCGGACCCAGGATGC	3038
Db	1899	GGATGTGATGGCGAGCGCCCGGCNCTGGAACTGTCTGCTACGAGGAGAGGCTTGAGAG	1958				

QY 1870 aLeuGlnGlnArgProSerValLeuHisLeuThrGlyMetLeuGlyLeuThrAlaVal 1890
DB 3039 CTTCCAGCAGACCACTGCTTCAACACAGGATGAAGGATATCATCACCGCTGT 3098
QY 1890 lGluProSerLysProThrValLeuArgSerThrSerSerProValArgProAl 1910
DB 3099 GAGGCCAGCAAGCCACCGTCTGAGGTCCACCTCCACCTCTCCACCGGTTCGCCAGC 3158
QY 1910 aAlaThrPheProAlaThrHisCyEP-roLeuGlyGlyThrLeuAspGlyValTyPr 1930
DB 3159 TGCCACATTTCCACCTGCCACCCACTGCCACTGGGCGGCACTCGATGGGGTCTACCC 3218
QY 1930 oThrLeuMetGluProValLeuLeuProLysGluAlaProArgValAlaArgProGluAr 1950
DB 3219 TACCTCTCATGGAGCCCGTCTTGTGCTCCCAAGAGGCCGCCCGGGTCCGCCGCCAGAGCG 3278
QY 1950 gProArgAlaAspThrGlyHisAlaPheLeuAlaLysProAlaArgSerGlyLeuG1 1970
DB 3279 GCCCGGAGCAGACACCGGCTTCTGCTGCCCAAGCCGCCAGCCGCTCCGGGCTGGA 3338
QY 1970 uProAlaSerSerProSerLysGlySerGluProArgProLeuValProProValSerG1 1990
DB 3339 GCCCGCTCTCTCCCGCAGAGGGCTCGGAGCCCGGCTTGTGCTTCTGCTCTCTCTG 3398
QY 1990 yHisAlaThrLeuAlaArgThrProAlaLysAsnLeuAlaProHisHisAlaSerProAs 2010
DB 3399 CACGCGCACCATCGCCGCCACCCCTCGCAAGAACCTCGCACCTCACCAAGCCGCCCGGA 3458
QY 2010 pProProAlaProProAlaSerAlaSerAspProHisArgGluLysThrGlnSerLysPr 2030
DB 3459 CCGCGCGCGCCACTGCTGCTCGACCCGCGCGGAGGAGGCTCAAGGTAAACC 3518
QY 2030 oPheSerileGlnLeuLeuLeuArgSerLeuGlyTyHisGlySerSerTySerPr 2050
DB 3519 CTTTTCATPCAGAGACTGGAACTCCGTTCTCTGGGTTTACCGGCGAGCAGCTACAGCCC 3578
QY 2050 oGluGlyValGluProValSerProValSerProSerLeuThrHisAspLysGlyLe 2070
DB 3579 CGAAGGGTGGAGCCGCTGAGCCCTGTGAGCTCACCCAGCTGACCCACCAAGGGGCT 3638
QY 2070 uProLysHisLeuGluLeuAspLysSerHisLeuGluGlyGluLeuArgProLysG1 2090
DB 3639 CCCCAGCACCTCGAAGAGCTCGACAGAGCCACTCGAGGGGGAGCTGCGGCCAGCA 3698
QY 2090 nProGlyProValLysLeuGlyGlyAlaAlaHisLeuProHisLeuArgProLeuPr 2110
DB 3699 GCCAGGCCCGTGAGCTTGGCGGGAGCGGCCCACTCCACACTGCGCGCGCTGCC 3758
QY 2110 oGluSerGlnProSerSerProLeuLeuGlnThrAlaProGlyValLysGlyHisG1 2130
DB 3759 TGAGAGCCAGCCCTGCTGTCAGCCGCTGCTCCAGACCCGCCCGCCAGGGGTCAAAGGTCA 3818
QY 2130 nArgValValThrLeuAlaGlnHisIleSerGluValIleThrGlnAspTyThrArgH1 2150
DB 3819 GGGGTGTCTACCTTGCCCGCAGCATCATGTGAGGTCTATCACAGGACTACACCCGCA 3878
QY 2150 sHisProGlnLeuSerAlaProLeuProAlaProLeuTySerPheProGlyAlaSe 2170
DB 3879 CCACCCACAGCAGCTCAGCGCACCTGCGCGCCCTGCGCGCCCTCTACTCTTCCCTGGGGCCAG 3938
QY 2170 rCySProValLeuAspLeuArgProProSerAspLeuTyLeuProProProAspH1 2190
DB 3939 CTGCCCCGTCTGACCTCGCGCGCCACCCAGGTGACTCTACTCTCCCGCCCGCCGACCA 3998
QY 2190 sGlyAlaProAlaArgGlySerProHisSerGluGlyGlyLysArgSerProGluProAs 2210
DB 3999 TGTGCCCCCGCGCTGGCTTCCCCCAGCAGAGGGGCGCAGAGGTCTCCAGAGCCCAA 4058
QY 2210 nLysThrSerValLeuGlyGlyGlyGluAspGlyLeuGluProValSerProProGluG1 2230
DB 4059 CAAAGACGTGCGTCTTGGGTGGTGGAGACGGTATTGAACCTGTGTCCCGCCAGCGAGG 4118
QY 2230 yMetThrGluProGlyHisSerArgSerAlaValTyProLeuLeuTyArgAspGlyG1 2250

DB 4119 CATGACGGAGCTGAGGCACTCCCGAGTGTGTGTACCCGCTGTGTACCGGATGGGA 4178
QY 2250 uGlnThrGluProSerArgMetGlySerLysSerProGlyAenThrSerGlnProProAl 2270
DB 4179 ACAGACGGAGCTCAGCAGGATGGCTCCAAGTCTCCAGGCAACACCCAGCAGCGCCAGC 4238
QY 2270 aPhePheSerLysLeuThrGluSerAsnSerAlaMetValLysSerLysLysGlnGlu1 2290
DB 4239 CTTCTTCAGCACTGACCGAGAGCACTCCGCTATGGTCAAGTCCAGAGCAAGAGAT 4298
QY 2290 eAsnLysLysLeuAsnThrHisAsnArgAsnGluProGluTyArgLysSerGlnProG1 2310
DB 4299 CACACAGAACCTCAACACACCGAATGAGCTGAATACATATATACGAGCAGCTGG 4358
QY 2310 yThrGluLeuPheAsnMetProAlaIleThrGlyThrGlyLeuMetThrTyArgSerG1 2330
DB 4359 GACGAGATCTTCAATATGCCCGCATCACCGGACAGGCTTTATGACCTATTAGAAGCCA 4418
QY 2330 nAlaValGlnGlnHisAlaSerThrAsnMetGlyLeuGluAlaIleLeuArgLysAlaLe 2350
DB 4419 GGCGGTGACAGGACATGCCAGCACCAATGGGGCTGGAGGCCATAATTAGAAGCACT 4478
QY 2350 uMetGlyLysTyAspGlnTrpGluGluSerProProLeuSerAlaAsnAlaPheAsnPr 2370
DB 4479 CATGGGTAAATATGACCAAGTGGGAGAGTCCCCCGGCTCAGCGCCAAATGCTTTTAAACC 4538
QY 2370 oLeuAsnAlaSerAlaSerLeuProAlaAlaMetProIleThrAlaAlaAspGlyArgSe 2390
DB 4539 TCTGATATGCATGTCAGGCTGCGCGCTGCTATGCTCCATTAACCTCTGACGAGCGAG 4598
QY 2390 rAspHisThrLeuThrSerProGlyGlyGlyLysAlaLysValSerGlyArgProSe 2410
DB 4599 TGACCAACACACTCACCTCGCAGGTGGCGCGGAGGCCCAAGGTCTCTGCGAGACCCAG 4658
QY 2410 rSerArgLysAlaLysSerProAlaProGlyLeuAlaSerGlyAspArgProProSerVa 2430
DB 4659 CAGCCGAAAGAGTAAGTCCCCCGGCGGCTGCGCATCTGGGACCGCGCCCTCTGT 4718
QY 2430 lSerSerValHisSerGluGlyAspCyAsnArgThrProLeuThrAsnArgValTr 2450
DB 4719 CTCTCATGTGCTCTCGAGGAGACTGCAACCGCGGAGCGCTTACCACCGCGGTGTG 4778
QY 2450 pGluAspArgProSerSerAlaGlySerThrProPheProTyArgProLeuLeuMetAr 2470
DB 4779 GAGAGCAGGCTCTGCTCCGAGGTTCCACGCACTTCCCTTACAAACCCCTGATCATGCG 4838
QY 2470 gLeuGlnAlaGlyValMetAlaSerProProProGlyLeuProAlaGlySerGlyPr 2490
DB 4839 GCTGACGCGGCTGTCTATGCTTCCACCCCGGCGCTCCCGCGGCGGCGGCGCC 4898
QY 2490 oLeuAlaGlyPheHisAlaTrpAspGluProLysProLeuLeuCySerGlnTy 2510
DB 4899 CTTGCTGCGCTCACACCGCTTGGGAGGAGGCCCAAGCCACTGCTTCTGCTGCGAGTA 4958
QY 2510 rGluThrLeuSerAspSerGlu 2517
DB 4959 CGAGACACTCTCGACAGCGAG 4980

RESULT 7
S83390
LOCUS
DEFINITION T3 receptor-associated cofactor-1 [human, fetal liver, mRNA, 2930 bp
ACCESSION S83390
VERSION S83390.1 GI:1511769
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM
REFERENCE
AUTHORS Sande, S. and Privalsky, M. L.

